

BLAST Basic Local Alignment Search Tool**Job Title: M18930:Human hepsin mRNA, complete cds**

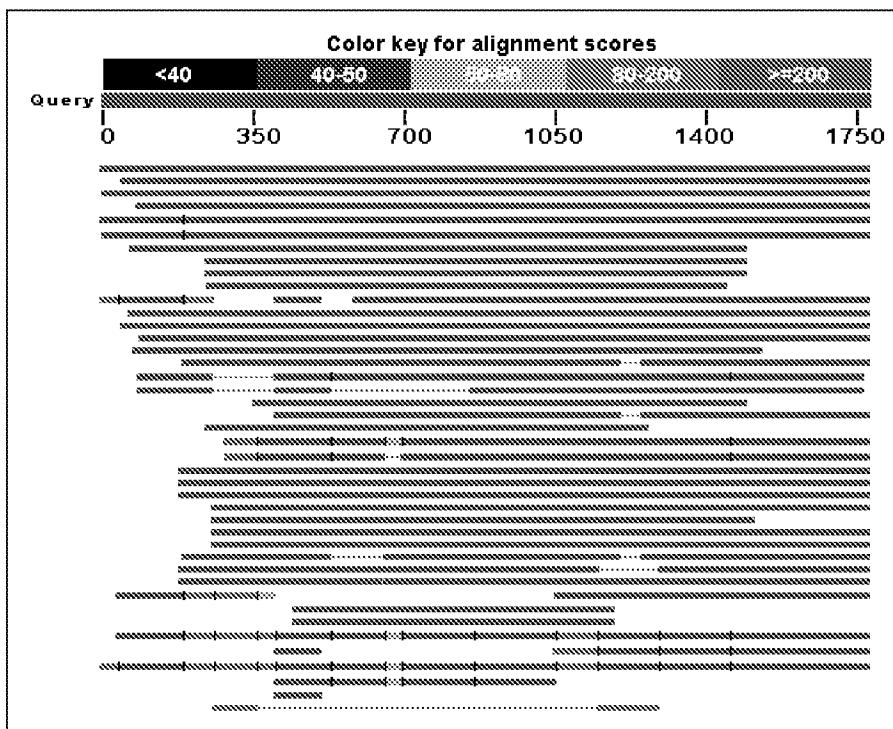
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BLASTN 2.2.18+

RID: 36C7FNM2013 Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences) 6,839,787 sequences; 23,768,953,950 total letters

Query= gi|184371|gb|M18930.1|HUMHPSNA Human hepsin mRNA, complete cds. Length=1783

Distribution of 106 Blast Hits on the Query Sequence

Distance tree of results [NEW](#)

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

NM_002151.1	Homo sapiens hepsin (transmembrane protease, serine 1) (HPN), transcript variant 2, mRNA >gb M18930.1 HUMHPSNA Human hepsin mRNA, complete cds	3293	3293	100%	0.0	100%	
BC025716.1	Homo sapiens hepsin (transmembrane protease, serine 1), mRNA (cDNA clone MGC:34588 IMAGE:5228525), complete cds	3199	3199	97%	0.0	99%	
XM_001093578.1	PREDICTED: Macaca mulatta hepsin (transmembrane protease, serine 1), transcript variant 2 (HPN), mRNA	3057	3057	99%	0.0	97%	
CR860913.1	Pongo abelii mRNA; cDNA DKFZp469A1831 (from clone DKFZp469A1831)	3000	3000	95%	0.0	98%	
NM_182983.1	Homo sapiens hepsin (transmembrane protease, serine 1) (HPN), transcript variant 1, mRNA >emb X07732.1 HSHEPSH Human hepatoma mRNA for serine protease hepsin	2942	3300	100%	0.0	100%	
XM_001093699.1	PREDICTED: Macaca mulatta hepsin (transmembrane protease, serine 1), transcript variant 3 (HPN), mRNA	2754	3063	99%	0.0	97%	
AK315655.1	Homo sapiens cDNA, FLJ96746	2645	2645	80%	0.0	100%	
DQ895314.2	Synthetic construct Homo sapiens clone IMAGE:100009774; FLH183201.01L; RZPDc839H04139D hepsin (transmembrane protease, serine 1) (HPN) gene, encodes complete protein	2309	2309	70%	0.0	99%	
DQ892119.2	Synthetic construct clone IMAGE:100004749; FLH183205.01X; RZPDc839H04140D hepsin (transmembrane protease, serine 1) (HPN) gene, encodes complete protein	2309	2309	70%	0.0	99%	
EU644753.1	Homo sapiens truncated hepsin serine protease mRNA, complete cds	2228	2228	67%	0.0	100%	
X07002.1	H.sapiens liver mRNA for serine protease hepsin	2215	2215	67%	0.0	100%	
AK233353.1	Sus scrofa mRNA, clone:LVRM10127D02, expressed in liver	2069	2069	96%	0.0	88%	
NM_001080241.2	Bos taurus hepsin (transmembrane protease, serine 1) (HPN), 1973 mRNA >gb BC140636.1 Bos taurus hepsin (transmembrane protease, serine 1), mRNA (cDNA clone MGC:148484 IMAGE:8196479), complete cds	1973	1973	97%	0.0	87%	
BT029913.1	Bos taurus hepsin (transmembrane protease, serine 1) (HPN), 1956 mRNA, complete cds	1956	1956	94%	0.0	87%	
XM_541697.2	PREDICTED: Canis familiaris similar to Serine protease hepsin (Transmembrane protease, serine 1) (LOC484583), mRNA	1873	1873	81%	0.0	89%	
XM_001157575.1	PREDICTED: Pan troglodytes hepsin (transmembrane protease, serine 1), transcript variant 2 (HPN), mRNA	1868	2836	86%	0.0	99%	
CR597177.1	full-length cDNA clone CS0DJ003YL08 of T cells (Jurkat cell 1714 line) Cot 10-normalized of Homo sapiens (human)	2852	86%	0.0	100%		
CR592189.1	full-length cDNA clone CS0DM012Y015 of Fetal liver of Homo sapiens (human)	1663	2235	68%	0.0	100%	
CU693029.1	Synthetic construct Homo sapiens gateway clone IMAGE:100019300 3' read HPN mRNA	1653	1653	64%	0.0	92%	
XM_001157514.1	PREDICTED: Pan troglodytes hepsin (transmembrane protease, serine 1), transcript variant 1 (HPN), mRNA	1476	2445	74%	0.0	99%	
CU693028.1	Synthetic construct Homo sapiens gateway clone IMAGE:100019300 5' read HPN mRNA	1465	1465	57%	0.0	92%	
AK095160.1	Homo sapiens cDNA FLJ37841 fis, clone BRSSN2012081, highly similar to SERINE PROTEASE HEPSIN (EC 3.4.21.-)	1404	2782	83%	0.0	100%	
XM_001093460.1	PREDICTED: Macaca mulatta hepsin (transmembrane protease, serine 1), transcript variant 1 (HPN), mRNA	1360	2552	81%	0.0	98%	
NM_008281.3	Mus musculus hepsin (Hpn), transcript variant 2, mRNA	1303	1303	89%	0.0	81%	
NM_017112.1	Rattus norvegicus hepsin (Hpn), mRNA >emb X70900.1 RNPHEPA R.norvegicus mRNA for hepsin	1297	1297	89%	0.0	81%	
AF030065.1	Mus musculus serine protease hepsin mRNA, complete cds	1280	1280	89%	0.0	81%	
NM_001110252.1	Mus musculus hepsin (Hpn), transcript variant 1, mRNA	1245	1245	85%	0.0	81%	
BC138809.1	Mus musculus hepsin, mRNA (cDNA clone MGC:170436 IMAGE:8861831), complete cds	1240	1240	70%	0.0	84%	
AK156553.1	Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830029I12 product:hepsin, full insert sequence	1240	1240	85%	0.0	81%	
AK002694.1	Mus musculus adult male kidney cDNA, RIKEN full-length	1181	1181	85%	0.0	81%	

	enriched library, clone:0610030A17 product:hepsin, full insert sequence								
XM_512584.2	PREDICTED: Pan troglodytes hepsin (transmembrane protease, serine 1), transcript variant 3 (HPN), mRNA	1011	2618	79%	0.0	100%			G
BC072688.1	Rattus norvegicus hepsin, mRNA (cDNA clone MGC:91742 IMAGE:7098661), complete cds	935	1200	82%	0.0	84%			G
AY234104.1	Mus musculus truncated hepsin splice variant mRNA, complete cds; alternatively spliced	880	1283	89%	0.0	82%			G
XM_001254640.1	PREDICTED: Bos taurus similar to hepsin (LOC787164), partial mRNA	815	815	41%	0.0	86%			G
BC119448.1	Mus musculus cDNA clone IMAGE:40044314	717	717	41%	0.0	84%			
BC119449.1	Mus musculus cDNA clone IMAGE:40044315	712	712	41%	0.0	84%			
AC192150.4	Pan troglodytes BAC clone CH251-522E19 from chromosome 19, complete sequence	590	3279	97%	9e-165	100%			
AK091988.1	Homo sapiens cDNA FLJ34669 fis, clone LIVER2001051	590	1367	41%	9e-165	100%			
AC020907.6	Homo sapiens chromosome 19 clone CTD-2527I21, complete sequence	590	3376	100%	9e-165	100%			
AK125670.1	Homo sapiens cDNA FLJ43682 fis, clone TBAES2001258, weakly similar to SERINE PROTEASE HEPSIN (EC 3.4.21.-)	353	1228	36%	1e-93	100%			
DQ677665.1	Homo sapiens sodium channel beta-1 subunit precursor (SCN1B) gene, complete cds	289	509	14%	4e-74	100%			
AC197610.3	MACACA MULATTA BAC clone CH250-348G8 from chromosome 19, complete sequence	250	637	20%	2e-62	98%			
XM_001719305.1	PREDICTED: Homo sapiens hypothetical protein LOC100128675 (LOC100128675), mRNA	207	207	6%	1e-49	100%			G
XM_001721961.1	PREDICTED: Homo sapiens hypothetical protein LOC100128675 (LOC100128675), mRNA	207	207	6%	1e-49	100%			G
XM_001719287.1	PREDICTED: Homo sapiens hypothetical protein LOC100128675 (LOC100128675), mRNA	207	207	6%	1e-49	100%			G
AC158993.2	Mus musculus BAC clone RP24-427N13 from chromosome 7, complete sequence	141	260	13%	1e-29	87%			

Alignments

>**ref|NM_002151.1|** Homo sapiens hepsin (transmembrane protease, serine 1) (HPN), transcript variant 2, mRNA

gb|M18930.1|HUMHPSNA Human hepsin mRNA, complete cds
Length=1783

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]
(Over 10 PubMed links)

Score = 3293 bits (1783), Expect = 0.0
Identities = 1783/1783 (100%), Gaps = 0/1783 (0%)
Strand=Plus/Plus

Query 1	TCGAGCCCGCTTCCAGGGACCCCTACCTGAGGGCCCAACAGGTGAGGGCAGCCTGGCCTAGC	60
Sbjct 1	TCGAGCCCGCTTCCAGGGACCCCTACCTGAGGGCCCAACAGGTGAGGGCAGCCTGGCCTAGC	60
Query 61	AGGCCCGACGCCACCGCCTCTGCCTCCAGGCCGCCCTGCTGCAGGGCCACCATGCTCC	120
Sbjct 61	AGGCCCGACGCCACCGCCTCTGCCTCCAGGCCGCCCTGCTGCAGGGCCACCATGCTCC	120
Query 121	TGCCCAAGGCTGGAGACTGACCCGACCCGGCACTACCTCGAGGCTCCGCCACCTGCG	180
Sbjct 121	TGCCCAAGGCTGGAGACTGACCCGACCCGGCACTACCTCGAGGCTCCGCCACCTGCG	180
Query 181	TGGACCCCAGGGTCCCACCCCTGGCCCAGGAGGTCAAGGCCAGGGAAATCATTAACAAGAGGCA	240
Sbjct 181	TGGACCCCAGGGTCCCACCCCTGGCCCAGGAGGTCAAGGCCAGGGAAATCATTAACAAGAGGCA	240
Query 241	GTGACATGGCGCAGAAGGAGGGTGGCCGGACTGTGCATGCTGCTCCAGACCCAAGGTGG	300
Sbjct 241	GTGACATGGCGCAGAAGGAGGGTGGCCGGACTGTGCATGCTGCTCCAGACCCAAGGTGG	300
Query 301	CAGCTCTCACTGCGGGGACCCCTGCTACTTCTGACAGGCCATGGGGCGGATCCTGGGCA	360
Sbjct 301	CAGCTCTCACTGCGGGGACCCCTGCTACTTCTGACAGGCCATGGGGCGGATCCTGGGCA	360
Query 361	TTGTGGCTGTTCTCCTCAGGAGTGACCAAGGAGCCGCTGTACCCAGTCAGGTCACTCTG	420
Sbjct 361	TTGTGGCTGTTCTCCTCAGGAGTGACCAAGGAGCCGCTGTACCCAGTCAGGTCACTCTG	420
Query 421	CGGACGCTCGGCTCATGGTCTTGAACAAGACGGAAGGGACGTGGCCGGCTGCTGTGCTCCT	480
Sbjct 421	CGGACGCTCGGCTCATGGTCTTGAACAAGACGGAAGGGACGTGGCCGGCTGCTGTGCTCCT	480
Query 481	CGCGCTCAAACGCCAGGGTAGCCGACTCAGTGCAGGGAGATGGGCTCCTCAGGGCAC	540
Sbjct 481	CGCGCTCAAACGCCAGGGTAGCCGACTCAGTGCAGGGAGATGGGCTCCTCAGGGCAC	540
Query 541	TGACCCACTCCGAGCTGGACGTGCGAACGGGGGCCAATGGCACGTGGCTTCTTCT	600
Sbjct 541	TGACCCACTCCGAGCTGGACGTGCGAACGGGGGCCAATGGCACGTGGCTTCTTCT	600
Query 601	GTGTGGACGAGGGGAGGCTGCCACACCCAGAGGCTGCTGGAGGTCACTCCGTGTGTG	660
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Query 721	CCGTGGACCGCATGTGGAGGCCGGACACCAGCTGGCCGGTGGCGTGGCAAGTCA	780
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Query 841	TGACAGCCGCCACTGCTCCGGAGCGGAACCGGGTCTGTCCCCATGGCGAGTGTGTTG	900
Sbjct 841	TGACAGCCGCCACTGCTCCGGAGCGGAACCGGGTCTGTCCCCATGGCGAGTGTGTTG	900
Query 901	CCGGTGCCGTGGCCCAAGGCCCTCTCCCCACGGCTCTGCAGCTGGGGTGCAGGCTGTGGCT	960
Sbjct 901	CCGGTGCCGTGGCCCAAGGCCCTCTCCCCACGGCTCTGCAGCTGGGGTGCAGGCTGTGGCT	960
Query 961	ACCACGGGGCTATCTCCCTTCCGGACCCAAACAGCGAGGAGAACAGCAACGATATTG	1020
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Query 1021	CCCTGGTCCACCTCTCCAGTCCCCCTGCCCTCACAGAACATCCAGCCTGTGTGCTCC	1080
Sbjct 1021	CCCTGGTCCACCTCTCCAGTCCCCCTGCCCTCACAGAACATCCAGCCTGTGTGCTCC	1080
Query 1081	CAGCTGCCGCCAGGGCTGGTGGATGGCAAGATCTGTACCGTGCAGGGCTGGGCAACA	1140
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Query 1141	CGCAGTACTATGGCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCATAATCAGCA	1200

Sbjct	1141	CGCAGTACTATGGCCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCA	1200
Query	1201	ATGATGTCGCAATGGCGCTGACTTCTATGAAACCAGATCAAGCCAAGATGTTCTGTG	1260
Sbjct	1201	ATGATGTCGCAATGGCGCTGACTTCTATGAAACCAGATCAAGCCAAGATGTTCTGTG	1260
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Query	1321	GTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGAGTTGGGCA	1380
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Query	1381	CTGGCTGTGCCCTGGCCCAGAAGCCAGGCCTACACCAAAGTCAGTGACTTCCGGAGT	1440
Sbjct	1381	CTGGCTGTGCCCTGGCCCAGAAGCCAGGCCTACACCAAAGTCAGTGACTTCCGGAGT	1440
Query	1441	GGATCTTCAGGCCATAAAGACTCACTCCGAAGCCAGCGCATGGTACCCAGCTTGAC	1500
Sbjct	1441	GGATCTTCAGGCCATAAAGACTCACTCCGAAGCCAGCGCATGGTACCCAGCTTGAC	1500
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Query	1681	CACCCCTCTGACCCCCATGTAATAATTGTTCTGCTGTCTGGACTCTGTCTAGGTGCC	1740
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Query	1741	CTGATGATGGGATGCTTTAAATAATAAAAGATGGTTTGATT	1783
Sbjct	1741	CTGATGATGGGATGCTTTAAATAATAAAAGATGGTTTGATT	1783

>gb|BC025716.1| Homo sapiens hepsin (transmembrane protease, serine 1), mRNA (cDNA clone MGC:34588 IMAGE:5228525), complete cds
Length=1761

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]
(Over 10 PubMed links)

Score = 3199 bits (1732), Expect = 0.0
Identities = 1734/1735 (99%), Gaps = 0/1735 (0%)
Strand=Plus/Plus

Query	49	GCCTGGCTAGCAGGCCAACGCCCTGCCCTCCAGGCCGCCGCTGCTGCCGGGG	108
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Sbjct	61	CCACCATGCTCTGCCAGGCCCTGGAGACTGACCCGACCCGGCACTACCTCGAGGCTCC	120
Query	169	GCCCCCACCTGCTGGACCCAGGGTCCACCCCTGGCCAGGAGGTAGCCAGGGAAATCAT	228
Sbjct	121	GCCCCCACCTGCTGGACCCAGGGTCCACCCCTGGCCAGGAGGTAGCCAGGGAAATCAT	180
Query	229	TAACAAGAGGCAGTGACATGGCGCAGAAGGGAGGTGGCGGACTGTGCATGCTGCC	288
Sbjct	181	TAACAAGAGGCAGTGACATGGCGCAGAAGGGAGGTGGCGGACTGTGCATGCTGCC	240
Query	289	GACCCAAGGGTGGCAGCTCTCACTGCCGGGACCCCTGCTACTCTGACAGCCATCGGGCGG	348
Sbjct	241	GACCCAAGGGTGGCAGCTCTCACTGCCGGGACCCCTGCTACTCTGACAGCCATCGGGCGG	300
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Query	409	AGGTCACTCTGCCAGCCTGGCTCATGGCTTTGACAAGACGGAAGGGACGGCGGG	468
Sbjct	361	AGGTCACTCTGCCAGCCTGGCTCATGGCTTTGACAAGACGGAAGGGACGGCGGG	420
Query	469	TGCTGTGCTCTGCCCTCCACGCCAGGGTAGCCGACTCAGCTGCCAGGAGATGGGCT	528
Sbjct	421	TGCTGTGCTCTGCCCTCCACGCCAGGGTAGCCGACTCAGCTGCCAGGAGATGGGCT	480
Query	529	TCCTCAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCCAATGGCACGT	588
Sbjct	481	TCCTCAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCCAATGGCACGT	540
Query	589	CGGGCTTCTCTGTGTGGACGAGGGAGGCTGCCACACCCAGAGGCTGCTGGAGGTCA	648
Sbjct	541	CGGGCTTCTCTGTGTGGACGAGGGAGGCTGCCACACCCAGAGGCTGCTGGAGGTCA	600
Query	649	TCTCCGTGTGATTGCCAGAGGCCCTTCTGGCCCATCTGCCAAGACTGTGGCC	708

Sbjct	601	TCTCCGTGTGATTGCCAGAGGCCGTTCTGGCCGCATCTGCCAAGACTGTGGCC	660
Query	709	GCAGGAAGCTGCCGTGGACCGCATCGTGGAGGCCGGACACCAGCTGGGCCGGTGGC	768
Sbjct	661	GCAGGAAGCTGCCGTGGACCGCATCGTGGAGGCCGGACACCAGCTGGGCCGGTGGC	720
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Sbjct	721	CGTGGCAAGTCAGCCTCGCTATGATGGAGCACACCTCTGTGGGGATCCCTGCTCTCG	780
Query	829	GGGACTGGGTGCTGACAGCCGCCACTGCTTCCCGAGCGGAACCGGGTCCGTCCCAG	888
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Sbjct	841	GGCGAGTGTGTTGCCGGTGGCGGAGGCCACGGCTCGCAGCTGGGGTGC	900
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Sbjct	1081	GCTGGGCAACACGAGTACTATGCCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCC	1140
Query	1189	CCATAATCAGCAATGATGCTGCAATGGCGCTGACTTCTATGAAACCAAGATCAAGCCA	1248
Sbjct	1141	CCATAATCAGCAATGATGCTGCAATGGCGCTGACTTCTATGAAACCAAGATCAAGCCA	1200
Query	1249	AGATGTTCTGTGCTGGTACCCGAGGGTGGCATTGATGCTGCCAGGGCGACAGCGGTG	1308
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Query	1369	TGAGTTGGGCACTGGCTGTGCCCTGGCCAGAAGCCAGCGTCAACCAAAGTCAGTG	1428
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Sbjct	1441	CCCAGCTCTGACCGGTGGCTCTCGCTGCGCAGCCTCCAGGGCCAGGTGATCCGGTG	1500
Query	1549	GTGGGATCCACGCTGGCCCGAGGATGGACCTTTCTCTTCTGGGGCCGTCCACAGGTG	1608
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Query	1729	GTCTAGGTGCCCTGATGGATGGGATGCTCTTAAATAATAAAAGATGGTTTGATT	1783
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>ref|XM_001093578.1| PREDICTED: Macaca mulatta hepsin (transmembrane protease, serine 1), transcript variant 2 (HPN), mRNA
Length=1785

GENE ID: 707242 HPN | hepsin (transmembrane protease, serine 1)
[Macaca mulatta]

Score = 3057 bits (1655), Expect = 0.0
Identities = 1739/1781 (97%), Gaps = 0/1781 (0%)
Strand=Plus/Plus

Query	3	GAGCCCGCTTCCAGGGACCCCTACCTGAGGGCCACAGGTGAGGCAGCCTGGCCTAGCAG	62
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Query	63	GCCCCACGCCACCGCCTCTGCCCTCAGGCCCGCCGCTGCTGCCGGGCCACCATGCTCTG	122
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Query	123	CCCAGGCCCTGGAGACTGACCCGACCCCGAACACCTCCAGGCTCCGCCCTCACCTGCCG	182
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Query	723	GTGGACCGCATCGTGGGAGGCCGGACACCAGCTTGGCCGGTGGCGTGGCAAGTCAGC	782
Sbjct	723	GTGGACCGCATCGTGGGAGGCCGGACACCAGCTTGGCCGGTGGCGTGGCAAGTCAGC	782
Query	783	CTTCGCTATGATGGAGCACACCTCTGTTGGGGATCCCTGCTCTCCGGGACTGGTGCTG	842
Sbjct	783	CTTCGCTATGATGGAGCACACCTCTGTTGGGGATCCCTGCTCTCCGGGACTGGTGCTG	842
Query	843	ACAGCCGCCACTGCTTCCGGAGCGGAACGGGTCTGTCCCAGTGGGAGTGTGGGCC	902
Sbjct	843	ACAGCTGCCACTGCTTCCGGAGCGGAACGGGTCTGTCCCAGTGGGAGTGTGGGCC	902
Query	903	GGTGCGGTGGCCAGGCCCTCTCCCCACGGCTCTGCAAGCTGGGGTGCAAGCTGTGGCTAC	962
Sbjct	903	GGTGCGGTGGCCAGGCCCTCTCCCCACGGCTCTGCAAGCTGGGGTGCAAGCTGTGGCTAC	962
Query	963	CACGGGGGCTATCTCCCTTCGGACCCAACAGCGAGGAGAACAGCAACGATAATTGCC	1022
Sbjct	963	CACGGGGGCTATCTCCCTTCGGACCCAACAGCGAGGAGAACAGCAATGATAATTGCC	1022
Query	1023	CTGGTCCACCTCTCCAGTCCCTGCCCTCACAGAACATCCAGCCTGTGCTCCCA	1082
Sbjct	1023	CTGGTCCACCTCTCCAGTCCCTGCCCTCACAGAACATCCAGCCTGTGCTCCCA	1082
Query	1083	GCTGCCGCCAGGCCCTGGTGGATGGCAAGATCTGACCGTGACGGGCTGGGGCACACG	1142
Sbjct	1083	GCTGCCGCCAGGCCCTGGTGGATGGCAAGATCTGACCGTGACGGGCTGGGGCACACG	1142
Query	1143	CAGTACTATGGCCAACAGGCCGGGGTACTCCAGGAGGCTGAGTCCCCATAATCAGCAAT	1202
Sbjct	1143	CAGTACTATGGCCAACAGGCCGGGGTACTCCAGGAGGCTGAGTCCCCATAATCAGCAAT	1202
Query	1203	GATGTCTGCAATGGCGCTGACTTCTATGGAAACCAAGATCAAGGCCAACATGGTCTGTGCT	1262
Sbjct	1203	GATGTCTGCAATGGCGCTGACTTCTATGGAAACCAAGATCAAGGCCAACATGGTCTGTGCT	1262
Query	1263	GGCTACCCCGAGGGTGGCATTGATGCCCTGCCAGGGCGACAGCGGTGGTCCCTTGTGT	1322
Sbjct	1263	GGCTACCCCGAGGGTGGCATTGATGCCCTGCCAGGGTGACAGCGGTGGTCCCTTGTGT	1322
Query	1323	GAGGACAGCATCTCTGGACGCCACGGTGGCGCTGTGTGCAAGTGGCTGGGACT	1382
Sbjct	1323	GAGGACAGCATCTCTGGACGCCACGGTGGCGCTGTGTGCAAGTGGCTGGGACT	1382
Query	1383	GGCTGTGCCCTGGCCAGAGCCAGGGCTACACCAAAGTCAGTGACTTCCGGAGTGG	1442
Sbjct	1383	GGCTGTGCCCTGGCCAGAGCCAGGGCTACACCAAAGTCAGTGACTTCCGGAGTGG	1442
Query	1443	ATCTTCCAGGCCATAAGACTCACTCCGAAGCCAGCGGCATGGTACCCAGCTCTGACCG	1502
Sbjct	1443	ATCTTCCAGGCCATAAGACTCACTCCGAAGCCAGCGGCATGGTACCCAGCTCTGACCG	1502
Query	1503	GTGGCTTCTCGCTGCGCAGCCTCAGGGCCCGAGGTGATCCGGTGGTGGATCCACGCT	1562
Sbjct	1503	GTGGCTTCTCGCTGCGCAGCCTCAGGGCCCGAGGTGATCCGGTGGTGGATCCACGCT	1562
Query	1563	GGGCCGAGGATGGGACGTTTCTCTGGGCCGGTCCACAGGTCAAGGACACCCCTCC	1622
Sbjct	1563	GGGCCGAGGATGGGACGTTTCTCTGGGCCGGTCCACAGGTCAAGGACACCCCTCC	1622
Query	1623	CTCCAGGGTCTCTTCCACAGTGGCGGGCCACTCAGCCCCGAGGACACCCAACTCA	1682

Sbjct	1623	CTCCAGGGTCCCTTCTTCCACAGTGGCGGGCCACTCAGCCCCGAGACCACCCGACCTCA	1682
Query	1683	CCCTCCTGACCCCCATGTAAATATTGTTCTGCTGTCTGGGACTCTCTGTCTAGGTGCCCT	1742
Sbjct	1683	CCCTCCTGACCCCCATGTAAATATTGTTCTGCTGTCTGGGACTCTCTGTCTAGGTGCCCT	1742
Query	1743	GATGATGGGATGCTCTTAAATAAAAGATGGTTTGATT	1783
Sbjct	1743	GATGACGGGATGCTCTTAAATAAAAGATGGTTTGATT	1783

>emb|CR860913.1| Pongo abelii mRNA; cDNA DKFZp469A1831 (from clone DKFZp469A1831)
Length=1741

Score = 3000 bits (1624), Expect = 0.0
Identities = 1676/1702 (98%), Gaps = 0/1702 (0%)
Strand=Plus/Plus

Query	82	GCCTCCAGGCCGCCGCTGCTGCGGGGCCACCATGCTCCTGCCAGGCCTGGAGACTGAC	141
Sbjct	18	GCCTCCAGGCCGCCGCTGCTGCGGGGCCACCATGCTCCTGCCAGGCCTGGAGACTGAC	77
Query	142	CCGACCCCGCACTACCTCGAGGCTCCGCCCCACCTGCTGGACCCAGGGTCCCACCC	201
Sbjct	78	CCGACCCCGCACTACCTCGAGGCTCCGCCCCACCTGCTGGACCCAGGGTCCCACCC	137
Query	202	GGCCCAGGAGGTCAGCCAGGGAACTATTAAACAAGAGGCAGTGACATGGCGCAGAAGGAGG	261
Sbjct	138	GGCCCAGGAGGTCAGCCAGGGAACTATTAAACAAGAGGCAGTGACATGGCGCAGAAGGAGG	197
Query	262	GTGGCCGGACTGTGCCATGCTGCTCCAGACCCAAGGTGGCAGCTCTCACTGCGGGGACCC	321
Sbjct	198	GTGGCCGGACTGTGCCATGCTGCTCCAGACCCAAGGTGGCAGCTCTCACTGCGGGGACCC	257
Query	322	TGCTACTCTGACAGCCATCGGGCGGCATCCTGGGCCATTGTGGCTGTTCTCCTCAGGA	381
Sbjct	258	TGCTACTCTGACAGCCATCGGGCGGCATCCTGGGCCATTGTGGCTGTTCTCCTCAGGA	317
Query	382	GTGACCAGGAGCCGTGACCCAGTCAGTCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCT	441
Sbjct	318	GTGACCAGGAGCCGTGACCCAGTCAGTCAGGTCAGCTCTGCGGACGCTCGGCTCATGGTCT	377
Query	442	TTGACAAGACGGAAGGGACGTGGCGGTGCTGTGCTCTCGCGCTCAAACGCCAGGGTAG	501
Sbjct	378	TTGACAAGACGGAAGGGACGTGGCGGTGCTGTGCTCTCGCGCTCAAACGCCAGGGTAG	437
Query	502	CCGGACTCAGCTGCGAGGAGATGGCTCCCTCAGGGCACTGACCCACTCCGAGCTGGACG	561
Sbjct	438	CCGGACTCAGCTGCGTGGAGATGGCTCCCTCAGGGCGTGAACCCACTCCGAGCTGGACG	497
Query	562	TGCGAACGGCGGGCGCAATGGCACGTGGCTTCTTCTGTGTGGACGAGGGGAGGCTGC	621
Sbjct	498	TGCGAACGGCGGGCGCAACGGCACGTGGCTTCTTCTGTGTGGACGAGGGGAGGCTGC	557
Query	622	CCCACACCAAGAGGCTGCTGGAGGTATCTCCGTGTGATTGCCAGAGGGCGTTCT	681
Sbjct	558	CCCACACCAAGAGGCTGCTGGAGGTATCTCCGTGTGATTGCCAGAGGGCGTTCT	617
Query	682	TGGCCGCCATCTGCCAAGACTGTGGCCGCAGGAAGCTGCCGTGGACCGCATGTGGAG	741
Sbjct	618	TGGCCGCCATCTGCCAAGACTGTGGCCGCAGGAAGCTGCCGTGGACCGCATGTGGAG	677
Query	742	GCCGGGACACCAAGCTGGCGGTGGCGTGGCAAGTCAGCCTTCGCTATGATGGAGCAC	801
Sbjct	678	GCCGGGACACCAAGCTGGCGGTGGCGTGGCAAGTCAGCCTTCGCTATGATGGAGCAC	737
Query	802	ACCTCTGTGGGGGATCCCTGCTCCGGGACTGGGTGCTGACAGGGCCCACTGCTTCC	861
Sbjct	738	ACCTCTGTGGGGGATCCCTGCTCCGGGACTGGGTGCTGACAGGGCCCACTGCTTCC	797
Query	862	CGGAGCGAACCGGGTCTGTCCGATGGCGAGTGTGTTGCCGTGGCGTGGCCAGGCCT	921
Sbjct	798	CAGAGCGAACCGGGTCTGTCCGATGGCGAGTGTGTTGCCGTGGCGTGGCCAGGCCT	857
Query	922	CTCCCCACGGCTCTGCAAGCTGGGGTGTGGCTACACAGGGGCTATCTCCCT	981
Sbjct	858	CTCCCCACGGCTCTGCAAGCTGGCGTGGCGTGTGGCTACACAGGGGCTATCTCCCT	917
Query	982	TTCGGGACCCAAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCACCTCTCCAGTC	1041
Sbjct	918	TTCGGGACCCAAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCACCTCTCCAGTC	977
Query	1042	CCCTGCCCTCACAGAATACATCCAGCTGTGCTGCCAGCTGCCAGGGCCAGGCCTGG	1101
Sbjct	978	CCCTGCCCTCACAGAATACATCCAGCTGTGCTGCCAGCTGCCAGGGCCAGGCCTGG	1037
Query	1102	TGGATGGCAAGATCTGTACCGTGACGGGCTGGGCAACAGCAGTAATGGCAACAGG	1161
Sbjct	1038	TGGATGGCAAGATCTGTACCGTGACGGGCTGGGCAACAGCAGTAATGGCAACAGG	1097
Query	1162	CCGGGGTACTCCAGGAGGCTGAGTCCCCATAATCAGCAATGATGTGCAATGGCGCTG	1221
Sbjct	1098	CCGGGGTACTCCAGGAGGCTGAGTCCCCATAATCAGCAATGATGTGCAATGGCGCTG	1157
Query	1222	ACTTCTATGGAAACCGAGATCAAGCCCAAGATGTTCTGTGCTGGTACCCCGAGGGTGGCA	1281
Sbjct	1158	ACTTCTATGGAAACCGAGATCAAGCCCAAGATGTTCTGTGCTGGTACCCCGAGGGTGGCA	1217

Query	1282	TTGATGCCCTGCCAGGGCGACAGCGGTGGTCCCTTGTGTGAGGAACAGCATTCTCGGA	1341
Sbjct	1218	TTGATGCCCTGCCAGGGCGACAGCGGTGGTCCCTTGTGTGAGGAACAGCATTCTCGGA	1277
Query	1342	CGCCACGTTGGCGGCTGTGGCATTGTGAGTTGGGCACTGGCTGTGCCCTGGCCCAGA	1401
Sbjct	1278	CGCCACGTTGGCGGCTGTGGCATTGTGAGCTGGGCACTGGCTGTGCCCTGGCCCAGA	1337
Query	1402	AGCCAGCGCTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTCCAGGCCATAAGA	1461
Sbjct	1338	AGCCAGCGCTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTCCAGGCCATAAGA	1397
Query	1462	CTCACTCGAAGCCAGCGCATGGTGACCCAGCTCTGACCGTGGCTTCGCTGCGCAG	1521
Sbjct	1398	CTCATTCCGAAGCCAGCGCATGGTGACCCAGCTCTGACCGTGGCTTCGCTGCGCAG	1457
Query	1522	CCTCCAGGGCCCGAGGTGATCCCGGTGGGGATCCAAGCCTGGGCCAGGGATGGGACGTT	1581
Sbjct	1458	CCTCCAGGGCCCGAGGTGATCTGGTGGGGATCCAAGCCTGGGCCAGGGATGGGACGTT	1517
Query	1582	TTTCTTCTTGGGCCGGTCCACAGGTCCAAGGACACCCCTCCAGGGTCCTCTTCC	1641
Sbjct	1518	TTTCTTCTTGGGCCGGTCCACAGGTCCAAGGACACCCCTCCAGGGTCCTCTTCC	1577
Query	1642	ACAGTGGCGGGCCCCTCAGCCCCGAGACCACCCAAACCTCACCCCTCTGACCCCCATGTA	1701
Sbjct	1578	ACAGTGGCGGGCCCCTCAGCCCCGAGACCACCCAAACCTCACCCCTGACCCCCATGTA	1637
Query	1702	AATATTGTTCTGCTGTCTGGGACTCTGTCTAGGTGCCCTGATGATGGGATGCTCTTA	1761
Sbjct	1638	AATATTGTTCTGCTGTCTGGGACTCTGTCTAGGTGCCCTGATGACGGGATGCTCTTA	1697
Query	1762	AATAATAAAAGATGGTTTGATT	1783
Sbjct	1698	AGTAATAAAAGATGGTTTGATT	1719

>ref|NM_182983.1| Homo sapiens hepsin (transmembrane protease, serine 1) (HPN), transcript variant 1, mRNA
emb|X07732.1|HSHEPSh Human hepatoma mRNA for serine protease hepsin
Length=2363

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]
(Over 10 PubMed links)

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 2942 bits (1593), Expect = 0.0
Identities = 1593/1593 (100%), Gaps = 0/1593 (0%)
Strand=Plus/Plus
Query 191 GGTCCCACCTGGCCCAGGGTCAGCCAGGGAACTTAAACAAGAGGCAGTGACATGGC 250
Sbjct 771 GGTCCCACCTGGCCCAGGGTCAGCCAGGGAACTTAAACAAGAGGCAGTGACATGGC 830
Query 251 GCAGAAAGGGGGTGGCCGACTGTGCCATGCTGCTCCAGACCCAAGGTGGCAGCTCTCAC 310
Sbjct 831 GCAGAAAGGGGGTGGCCGACTGTGCCATGCTGCTCCAGACCCAAGGTGGCAGCTCTCAC 890
Query 311 TGCGGGGACCTGCTACTTCTGACAGCCATCGGGGCGGATCTGGCCATTGTGGCTGT 370
Sbjct 891 TGCGGGGACCTGCTACTTCTGACAGCCATCGGGGCGGATCTGGCCATTGTGGCTGT 950
Query 371 TCTCCTCAGGAGTGACCAAGGGAGCGCTGTACCCAGTGCAGGTCAAGCTTGCGGACGCTCG 430
Sbjct 951 TCTCCTCAGGAGTGACCAAGGGAGCGCTGTACCCAGTGCAGGTCAAGCTTGCGGACGCTCG 1010
Query 431 GCTCATGGCTTTGACAAGACGAAAGGGACCTGGCGGCTGCTGTGCTCTCGCGCTCCAA 490
Sbjct 1011 GCTCATGGCTTTGACAAGACGAAAGGGACCTGGCGGCTGCTGTGCTCTCGCGCTCCAA 1070
Query 491 CGCCAGGGTAGCCGACTCAGCTGCGAGGGAGATGGGCTTCCTCAGGGACTGACCCACTC 550
Sbjct 1071 CGCCAGGGTAGCCGACTCAGCTGCGAGGGAGATGGGCTTCCTCAGGGACTGACCCACTC 1130
Query 551 CGAGCTGGACGTGCGAACGGCGGGCGCAATGGCACGTGGCTTCTGTGTGGACGA 610
Sbjct 1131 CGAGCTGGACGTGCGAACGGCGGGCGCAATGGCACGTGGCTTCTGTGTGGACGA 1190
Query 611 GGGGAGGCTGCCACACCCAGAGGCTGCTGGAGGTCACTCCGTGTGATTGCCAG 670
Sbjct 1191 GGGGAGGCTGCCACACCCAGAGGCTGCTGGAGGTCACTCCGTGTGATTGCCAG 1250
Query 671 AGGCCGTTCTGGCCGCATCTGCCAAGACTGTGGCGCAGGAAGCTGCCGTGGACCG 730
Sbjct 1251 AGGCCGTTCTGGCCGCATCTGCCAAGACTGTGGCGCAGGAAGCTGCCGTGGACCG 1310
Query 731 CATCGTGGAGGCCGGACACCGACTTGGCGGTGGCGTGGCAAGTCAGCCTCGCTA 790
Sbjct 1311 CATCGTGGAGGCCGGACACCGACTTGGCGGTGGCGTGGCAAGTCAGCCTCGCTA 1370
Query 791 TGATGGAGCACACCTCTGTGGGGATCCCTGCTCCGGGACTGGGTGCTGACAGCCG 850
Sbjct 1371 TGATGGAGCACACCTCTGTGGGGATCCCTGCTCCGGGACTGGGTGCTGACAGCCG 1430

Query	851	CCACTGCTTCCGGAGCGGAACGGGTCTGTCCCAGATGGCAGTGTTGCCGGTGCCTG	910
Sbjct	1431	CCACTGCTTCCGGAGCGGAACGGGTCTGTCCCAGATGGCAGTGTTGCCGGTGCCTG	1490
Query	911	GGCCCAGGCTCTCCCCACGGTCTGCAGCTGGGGTGCAGGCTGTGGTCTACCACGGGG	970
Sbjct	1491	GGCCCAGGCTCTCCCCACGGTCTGCAGCTGGGGTGCAGGCTGTGGTCTACCACGGGG	1550
Query	971	CTATCTTCCTTCGGACCCAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCA	1030
Sbjct	1551	CTATCTTCCTTCGGACCCAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCA	1610
Query	1031	CCTCTCAGTCCCCTGCCCTCACAGAATACTCCAGCCTGTGTGCCCTCCAGCTGCCG	1090
Sbjct	1611	CCTCTCAGTCCCCTGCCCTCACAGAATACTCCAGCCTGTGTGCCCTCCAGCTGCCG	1670
Query	1091	CCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGCTGGGAAACACGCAGTACTA	1150
Sbjct	1671	CCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGCTGGGAAACACGCAGTACTA	1730
Query	1151	TGGCCAACAGGCCGGGTAECTCAGGAGGCTCGAGTCCCATAATCAGCAATGATGTCTG	1210
Sbjct	1731	TGGCCAACAGGCCGGGTAECTCAGGAGGCTCGAGTCCCATAATCAGCAATGATGTCTG	1790
Query	1211	CAATGGCGCTGACTTCTATGGAAACAGATCAAGCCAAGATGTTCTGTGTGGTACCC	1270
Sbjct	1791	CAATGGCGCTGACTTCTATGGAAACAGATCAAGCCAAGATGTTCTGTGTGGTACCC	1850
Query	1271	CGAGGGTGGCATTGATGCTGCGCAGGGCGACAGCGGTGGTCCCTTGTGTGAGGACAG	1330
Sbjct	1851	CGAGGGTGGCATTGATGCTGCGCAGGGCGACAGCGGTGGTCCCTTGTGTGAGGACAG	1910
Query	1331	CATCTCTGGACGCCACGGTGGCGCTGTGTGGCATTTGTGAGTTGGGACTGGCTGTGC	1390
Sbjct	1911	CATCTCTGGACGCCACGGTGGCGCTGTGTGGCATTTGTGAGTTGGGACTGGCTGTGC	1970
Query	1391	CCTGGCCAGAAGCCAGCGTCTACACCAAAGTCAGTGACTTCCGGAGTGGATCTTCCA	1450
Sbjct	1971	CCTGGCCAGAAGCCAGCGTCTACACCAAAGTCAGTGACTTCCGGAGTGGATCTTCCA	2030
Query	1451	GGCCATAAAGACTCACTCCGAAGCCAGCGGATGGTACCCAGCTGACCGGTGGCTTC	1510
Sbjct	2031	GGCCATAAAGACTCACTCCGAAGCCAGCGGATGGTACCCAGCTGACCGGTGGCTTC	2090
Query	1511	TCGCTGCGCAGCCTCCAGGGCCGAGGTGATCCGGTGGTGGATCCACGCTGGCCGAG	1570
Sbjct	2091	TCGCTGCGCAGCCTCCAGGGCCGAGGTGATCCGGTGGTGGATCCACGCTGGCCGAG	2150
Query	1571	GATGGGACGTTTTCTTCTGGGCCGGTCCACAGGTCCAAGGACACCCCTCCCTCAGGG	1630
Sbjct	2151	GATGGGACGTTTTCTTCTGGGCCGGTCCACAGGTCCAAGGACACCCCTCCCTCAGGG	2210
Query	1631	TCCCTCTTCCACAGTGGCGGCCACTCAGCCCCGAGACCAACCTCACCTCCTG	1690
Sbjct	2211	TCCCTCTTCCACAGTGGCGGCCACTCAGCCCCGAGACCAACCTCACCTCCTG	2270
Query	1691	ACCCCCATGTAAAATTGTTCTGCTGTGGACTCTGTCTAGGTGCCCCGTGATGATGG	1750
Sbjct	2271	ACCCCCATGTAAAATTGTTCTGCTGTGGACTCTGTCTAGGTGCCCCGTGATGATGG	2330
Query	1751	GATGCTCTTAAATAAAAGATGGTTTGATT	1783
Sbjct	2331	GATGCTCTTAAATAAAAGATGGTTTGATT	2363

Score = 357 bits (193), Expect = 1e-94
 Identities = 193/193 (100%), Gaps = 0/193 (0%)
 Strand=Plus/Plus

Query	1	TCGAGCCGCTTCCAGGGACCTACCTGAGGGCCACAGGTGAGGCAGCCTGGCTAGC	60
Sbjct	1	TCGAGCCGCTTCCAGGGACCTACCTGAGGGCCACAGGTGAGGCAGCCTGGCTAGC	60
Query	61	AGGCCCAACGCCACCGCCTCTGCCCTCAGGCCGCCGCTGCTGCCGGCACATGCTCC	120
Sbjct	61	AGGCCCAACGCCACCGCCTCTGCCCTCAGGCCGCCGCTGCTGCCGGCACATGCTCC	120
Query	121	TGCCCAGGCCGGAGACTGACCCGACCCCGGCACTACCTCGAGGCTCCGCCACCTGC	180
Sbjct	121	TGCCCAGGCCGGAGACTGACCCGACCCCGGCACTACCTCGAGGCTCCGCCACCTGC	180
Query	181	TGGACCCAGGGT	193
Sbjct	181	TGGACCCAGGGT	193

>ref|XM_001093699.1| PREDICTED: Macaca mulatta hepsin (transmembrane protease, serine 1), transcript variant 3 (HPN), mRNA
 Length=2363

GENE ID: 707242 HPN | hepsin (transmembrane protease, serine 1)
 [Macaca mulatta]

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position

Score = 2754 bits (1491), Expect = 0.0
 Identities = 1559/1593 (97%), Gaps = 0/1593 (0%)
 Strand=Plus/Plus

Query 191	GGTCCCACCTGGCCAGGAGGTCAAGCAGGGAAATCATTAACAAGAGGCAGTGACATGGC	250
Sbjct 769	GGTCCCACCTGGCCAGGAGGTCAAGCAGGGAAATCATTAACAAGAGGCAGTGACATGGC	828
Query 251	GCAGAAGGAGGGTGGCCGGACTGTGCCATGCTGCTCAGACCCAAGGTGGCAGCTCTCAC	310
Sbjct 829	GCAGAAGGAGGGTGGCCGGACTGTGCCATGCTGCTCAGACCCAAGGTGGCAGCTCTCAC	888
Query 311	TGCAGGGACCTGCTACTTCTGACAGCCATCGGGCGGCATCTGGGCATTGTGGCTGT	370
Sbjct 889	TGCAGGGACCTGCTACTTCTGACAGCCATCGGGCGGCATCTGGGCATTGTGGCTGT	948
Query 371	TCTCCTCAGGAGTGAACAGGAGCGCTGTACCCAGTCAGGTCAGCTCGGGACGCTCG	430
Sbjct 949	TCTCCTCAGGAGTGAACAGGAGCGCTCTACCCAGTCAGGTCAGCTCGGGACGCTCG	1008
Query 431	GCTCATGGCTTTGACAAGACGGAAGGGACGTGGCGCTGCTGTGCTCTCGCGCTCCAA	490
Sbjct 1009	GCTCATGGCTTTGACAAGACGGAAGGGACGTGGCGCTGCTATGCTCTCACGCTCCAA	1068
Query 491	CGCCAGGGTAGCCGACTCAGCTGCGAGGAGATGGGCTTCTCAGGGCACTGACCCACTC	550
Sbjct 1069	CACCAGGGTAGCCGACTCAGCTGCGAGGAGATGGGCTTCTCAGGGCACTGACCCACTC	1128
Query 551	CGAGCTGGACGTGCGAACGGCGGCCAATGGCACGTCGGCTTCTCTGTGTGGACGA	610
Sbjct 1129	CGAGCTGGACGTGCGAACGGCGGCCAACGGCACGTCAGGCTTCTCTGTGTGGATGA	1188
Query 611	GGGGAGGCTGCCACACACCCAGAGGCTGCTGGAGGTACATCTCGTGTGATTGCCAG	670
Sbjct 1189	GGGGAGGCTGCCACACACCCAGAGGCTGCTGGAGGTACATCTCGTGTGACTGTCCCAG	1248
Query 671	AGGCCGTTCTGGCCGCATCTGCCAAGACTGTGGCCGAGGAAGCTGCCGTGGACCG	730
Sbjct 1249	AGGCCGTTCTGGCCACCGTCTGCCAAGACTGTGGCCGAGGAAGCTGCCGTGGACCG	1308
Query 731	CATCGTGGAGGCCGGACACCGACTTGGCCGGTGGCAAGTCAGCCTCGCTA	790
Sbjct 1309	CATCGTGGAGGCCGGACACCGACTTGGCCGGTGGCAAGTCAGCCTCGCTA	1368
Query 791	TGATGGAGCACACCTCTGTTGGGATCCCTGCTCTCCGGGACTGGGTGCTGACAGCCG	850
Sbjct 1369	TGATGGAGCACACCTCTGCGGGGGTCCCTGCTCTCCGGGACTGGGTGCTGACAGCTG	1428
Query 851	CCACTGCTCCGGAGCGAACCGGGTCTGTCCCGATGGCAGTGTTGCCGGTGGCGT	910
Sbjct 1429	CCACTGCTCCGGAGCGAACCGGGTCTGTCCCGATGGCAGTGTTGCCGGTGGCGT	1488
Query 911	GGCCCAAGGCCTCTCCCCACGGCTGCAAGCTGGGGTGCAGGCTGTGGCTACCAACGGGG	970
Sbjct 1489	GGCCCAAGGCCTCTCCCCACGGCTGCAAGCTGGGGTGCAGGCTGTGGCTACCAACGGGG	1548
Query 971	CTATCTCCCTTCGGGACCCCAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCA	1030
Sbjct 1549	CTATCTCCCTTCGGGACCCCAACAGCGAGGAGAACAGCAATGATATTGCCCTGGTCCA	1608
Query 1031	CCTCTCCAGTCCCCTGCCCTCACAGAATAACATCCAGCCTGTGTGCCCTCCAGCTGCCG	1090
Sbjct 1609	CCTCTCCAGTCCCCTGCCCTCACAGAATAACATCCAGCCTGTGTGCCCTCCAGCTGCTGG	1668
Query 1091	CCAGGCCCTGGTGGATGCCAAGATCTGTACCGTGACGGGCTGGGCAACACGCACTA	1150
Sbjct 1669	CCAGGCCCTGGTGGATGCCAAGATCTGTACCGTGACGGGCTGGGCAACACGCACTA	1728
Query 1151	TGGCCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTG	1210
Sbjct 1729	TGGCCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTG	1788
Query 1211	CAATGGCGCTGACTTCTATGGAAACAGATCAAGCCAAGATGTTCTGTGTGGCTACCC	1270
Sbjct 1789	CAATGGCGCTGACTTCTATGGAAACAGATCAAGCCAAGATGTTCTGTGTGGCTACCC	1848
Query 1271	CGAGGGTGGCATTGATGCCCTGCCAGGGTGACAGCGGTGGCCCTTGTGTGAGGACAG	1330
Sbjct 1849	CGAGGGTGGCATTGATGCCCTGCCAGGGTGACAGCGGTGGCCCTTGTGTGAGGACAG	1908
Query 1331	CATCTCTGGACGCCACGGTGGCGCTGTGTGCAAGGGCTGTGAGTTGGGGACTGGCTGTGC	1390
Sbjct 1909	CATCTCTGGACGCCACGGTGGCGCTGTGTGCAAGGGCTGTGAGCTGGGACTGGCTGTGC	1968
Query 1391	CCTGGCCCAGAACGCCAGGGCTACACCAAAGTCAGTGACTTCCGGAGTGGATCTTCCA	1450
Sbjct 1969	CCTGGCCCAGAACGCCAGGGCTACACCAAAGTCAGTGACTTCCGGAGTGGATCTTCCA	2028
Query 1451	GGCCATAAAAGACTCACTCCGAAGCCAGCGGCTGGTACGGGACTCTGACCGGTGGCTTC	1510
Sbjct 2029	GGCCATAAAAGACTCACTCCGAAGCCAGCGGCTGGTACGGGACTCTGACCGGTGGCTTC	2088
Query 1511	TCGCTGCGAAGCCTCCAGGGCCGGAGGTGATCCGGTGGGGATCCACGCTGGGCCAG	1570
Sbjct 2089	TCGCTGCGAAGCCTCCAGGGCCGGAGGTGATCTGGTGGGGATCCACGCTGGGCCAG	2148
Query 1571	GATGGGACGTTTCTTCTGGGCCGGTCCACAGGTCCAAGGACACCCCTCCAGGG	1630

			GATGGGACATTTCCTTGGGCCGGTCCACAGGTCCAAGGACACCCTCCCTCAGGG	2208
Sbjct	2149		TCCCTCTTCCACAGTGGGGCCACTCAGCCCCGAGACCACCAACCTCACCCCTCTG	1690
Query	1631		TCCCTTCCACAGTGGGGCCACTCAGCCCCGAGACCACCAACCTCACCCCTCTG	2268
			ACCCCCATGAAATATTGTTCTGCTGCTGGACTCTGTCTAGGTGCCCTGATGATGG	1750
Sbjct	2209		ACCCCCGTGAAATATTGTTCTGCTGCTGGACTCTGTCTAGGTGCCCTGATGACGG	2328
Query	1691		GATGCTCTTAAATAAAGATGGTTTGATT	1783
Sbjct	2269		GATGCTCTTAAATAAAGATGGTTTGATT	2361

Score = 309 bits (167), Expect = 3e-80
 Identities = 183/191 (95%), Gaps = 0/191 (0%)
 Strand=Plus/Plus

Query	3		GAGCCCGTTCCAGGGACCCCTACCTGAGGGCCACAGGTGAGGCAGCCTGGCCTAGCAG	62
Sbjct	3		GAGCCCGTTCCAGGGACCCCTACCCGAGGGCCACAGGTGAGGCAGCCTGGCCTAGCAG	62
Query	63		GCCCCACGCCACCGCCTCTGCCTCCAGGGCCCGCTGCTGCGGGGCCACCATGCTCCTG	122
Sbjct	63		GCCCCACGCCACCGCCTCTGCCTCCAGGGCCACCCGCTGCTGCGGGGCCACCATGCTCCTG	122
Query	123		CCCAGGCCTGGAGACTGACCGGACCCGGCACTACCTCGAGGCTCCGCCCAACCTGCTG	182
Sbjct	123		CCCAGGCCTGGAGACTGACCGGACCCGGAACCAACCTCCAGGCTCCGCCCTCACCTGCCG	182
Query	183		GACCCCCAGGGT	193
Sbjct	183		GACCCCCAGGGT	193

>dbj|AK315655.1| Homo sapiens cDNA, FLJ96746
 Length=1432

Score = 2645 bits (1432), Expect = 0.0
 Identities = 1432/1432 (100%), Gaps = 0/1432 (0%)
 Strand=Plus/Plus

Query	68		ACGCCACCGCCTCTGCCTCCAGGCCCGCCTGCTGCGGGGCCACCATGCTCTGCCAG	127
Sbjct	1		ACGCCACCGCCTCTGCCTCCAGGCCCGCCTGCTGCGGGGCCACCATGCTCTGCCAG	60
Query	128		GCCTGGAGACTGACCGGACCCCGGCACTACCTCGAGGCTCCGCCCACTGCTGGACCC	187
Sbjct	61		GCCTGGAGACTGACCGGACCCCGGCACTACCTCGAGGCTCCGCCCACTGCTGGACCC	120
Query	188		CAGGGTCCCACCCCTGGCCCAAGGAGGTCAGCCAGGGAAATCATTAAACAGAGGCAGTACAT	247
Sbjct	121		CAGGGTCCCACCCCTGGCCCAAGGAGGTCAGCCAGGGAAATCATTAAACAGAGGCAGTACAT	180
Query	248		GGCGCAGAAGGAGGGTGGCCGGAUTGTGCATGCTGCTCAGACCCAAGGTGGCAGCTCT	307
Sbjct	181		GGCGCAGAAGGAGGGTGGCCGGAUTGTGCATGCTGCTCAGACCCAAGGTGGCAGCTCT	240
Query	308		CACTGCGGGGACCCCTGCTACTTCTGACAGCCATCGGGCGGATCTGGCCATTGTGGC	367
Sbjct	241		CACTGCGGGGACCCCTGCTACTTCTGACAGCCATCGGGCGGATCTGGCCATTGTGGC	300
Query	368		TGTTCTCTCAGGAGTGAACAGGAGCCGCTGTACCCAGTCAGGTCACTCTGCCACGC	427
Sbjct	301		TGTTCTCTCAGGAGTGAACAGGAGCCGCTGTACCCAGTCAGGTCACTCTGCCACGC	360
Query	428		TCGGCTCATGGTCTTGAACAAGACGGAAGGGACGTGGCGCGCTGCTGTGCTCTCGCGCTC	487
Sbjct	361		TCGGCTCATGGTCTTGAACAAGACGGAAGGGACGTGGCGCGCTGCTGTGCTCTCGCGCTC	420
Query	488		CAACGCCAGGGTAGCCGACTCAGCTGCCAGGAGATGGCTTCTCAGGGCACTGACCCA	547
Sbjct	421		CAACGCCAGGGTAGCCGACTCAGCTGCCAGGAGATGGCTTCTCAGGGCACTGACCCA	480
Query	548		CTCCGAGCTGGACGTGCGAACGGCGGGCGCAATGGCACGTGGCGCTTCTGTGTGGA	607
Sbjct	481		CTCCGAGCTGGACGTGCGAACGGCGGGCGCAATGGCACGTGGCGCTTCTGTGTGGA	540
Query	608		CGAGGGGAGGGCTGCCACACCCAGAGGGCTGCTGGAGGTATCTCCGTGTGATTTGCC	667
Sbjct	541		CGAGGGGAGGGCTGCCACACCCAGAGGGCTGCTGGAGGTATCTCCGTGTGATTTGCC	600
Query	668		CAGAGGCCGTTCTTGGCCGCACTGCCAACAGACTGTGGCGCAGGAAGCTGCCGTGGA	727
Sbjct	601		CAGAGGCCGTTCTTGGCCGCACTGCCAACAGACTGTGGCGCAGGAAGCTGCCGTGGA	660
Query	728		CCGCATCGTGGAGGCCGGACACCAGCTTGGCCGGTGGCGTGGCAAGTCAGCCTTCG	787
Sbjct	661		CCGCATCGTGGAGGCCGGACACCAGCTTGGCCGGTGGCGTGGCAAGTCAGCCTTCG	720
Query	788		CTATGATGGAGCACACCTCTGTGGGGGATCCCTGCTCTCGGGGACTGGGTGCTGACAGC	847
Sbjct	721		CTATGATGGAGCACACCTCTGTGGGGGATCCCTGCTCTCGGGGACTGGGTGCTGACAGC	780
Query	848		CGCCCACTGCTCCGGAGCGGAACCGGGCTGTCCCGATGGCGAGTGTGTCGGTGC	907

Sbjct	781	CGCCCCACTGCTTCCGGAGCGGAACCGGGTCCTGTCCCAGATGGCGAGTGTTGCCGGTGC	840
Query	908	CGTGGCCCAGGGCTCTCCCCAACGGCTCGCAGCTGGGGTGCAGGCTGTGGCTAACACCGG	967
Sbjct	841	CGTGGCCCAGGGCTCTCCCCAACGGCTCGCAGCTGGGGTGCAGGCTGTGGCTAACACCGG	900
Query	968	GGGCTATCTCCCTTCCGGACCCAACAGCGAGGAGAACAGCAACGATATTGCCCTGGT	1027
Sbjct	901	GGGCTATCTCCCTTCCGGACCCAACAGCGAGGAGAACAGCAACGATATTGCCCTGGT	960
Query	1028	CCACCTCTCCAGTCCCCCTGCCCTCACAGAATAACATCCAGCCTGTGCTCCAGCTGC	1087
Sbjct	961	CCACCTCTCCAGTCCCCCTGCCCTCACAGAATAACATCCAGCCTGTGCTCCAGCTGC	1020
Query	1088	C GGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGCAACACCCAGTA	1147
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Query	1148	CTATGGCCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGT	1207
Sbjct	1081	CTATGGCCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGT	1140
Query	1208	CTGCAATGGCGCTGACTTCTATGGAAACCAGATCAAGCCAAGATGTTCTGTGCTGGCTA	1267
Sbjct	1141	CTGCAATGGCGCTGACTTCTATGGAAACCAGATCAAGCCAAGATGTTCTGTGCTGGCTA	1200
Query	1268	CCCCGAGGGTGGCATTGATGCCAGGGGACAGCGGTGGTCCCTTGTGAGGAA	1327
Sbjct	1201	CCCCGAGGGTGGCATTGATGCCAGGGGACAGCGGTGGTCCCTTGTGAGGAA	1260
Query	1328	CAGCATCTCGGACGCCACGTTGGCGCTGTGTGGCATTGTGAGTTGGGCACGGCTG	1387
Sbjct	1261	CAGCATCTCGGACGCCACGTTGGCGCTGTGTGGCATTGTGAGTTGGGCACGGCTG	1320
Query	1388	TGCCCTGGCCAGAACGCCAGGCGTACACAAAGTCAGTGACTTCCGGAGTGATCTT	1447
Sbjct	1321	TGCCCTGGCCAGAACGCCAGGCGTACACAAAGTCAGTGACTTCCGGAGTGATCTT	1380
Query	1448	CCAGGCCATAAAGACTCACTCGAACGCCAGGGCATGGTGACCCAGCTCTGA	1499
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>gb|DQ895314.2| Synthetic construct Homo sapiens clone IMAGE:100009774; FLH183201.01L; RZPD0839H04139D hepsin (transmembrane protease, serine 1) (HPN) gene, encodes complete protein Length=1294

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens] (Over 10 PubMed links)

Score = 2309 bits (1250), Expect = 0.0
 Identities = 1252/1253 (99%), Gaps = 0/1253 (0%)
 Strand=Plus/Plus

Query	245	CATGGCGCAGAAGGAGGGTGGCCGGACTGTGCCATGCTGCTCCAGACCCAAGGTGGCAGC	304
Sbjct	22	CATGGCGCAGAAGGAGGGTGGCCGGACTGTGCCATGCTGCTCCAGACCCAAGGTGGCAGC	81
Query	305	TCTCACTGCGGGGACCTGCTACTTCTGACAGCCATGGGGCGGCATCCTGGGCATTGT	364
Sbjct	82	TCTCACTGCGGGGACCTGCTACTTCTGACAGCCATGGGGCGGCATCCTGGGCATTGT	141
Query	365	GGCTGTTCTCTCAGGAGTGACCAGGAGCCGTGTACCCAGTGCAGGTAGCTCTGGGA	424
Sbjct	142	GGCTGTTCTCTCAGGAGTGACCAGGAGCCGTGTACCCAGTGCAGGTAGCTCTGGGA	201
Query	425	CGCTCGGCTCATGGCTTGTACAAGACGGAAGGGACGTGGCGCTGTGTGCTCCCTCGCG	484
Sbjct	202	CGCTCGGCTCATGGCTTGTACAAGACGGAAGGGACGTGGCGCTGTGTGCTCCCTCGCG	261
Query	485	CTCCAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGATGGGCTTCTCAGGGACTGAC	544
Sbjct	262	CTCCAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGATGGGCTTCTCAGGGACTGAC	321
Query	545	CCACTCCGAGCTGGACGTGCGAACGGCGGGCCTAACGGCACGTGGCTTCTCTGTGT	604
Sbjct	322	CCACTCCGAGCTGGACGTGCGAACGGCGGGCCTAACGGCACGTGGCTTCTCTGTGT	381
Query	605	GGACGAGGGAGGGCTGCCAACCCAGAGGTGCTGGAGGTCACTCCCGTGTGATTG	664
Sbjct	382	GGACGAGGGAGGGCTGCCAACCCAGAGGTGCTGGAGGTCACTCCCGTGTGATTG	441
Query	665	CCCCAGAGGCCGTTCTGGCCGCATCTGCCAACGACTGTGGCCGCAGGAAGCTGCCGT	724
Sbjct	442	CCCCAGAGGCCGTTCTGGCCGCATCTGCCAACGACTGTGGCCGCAGGAAGCTGCCGT	501
Query	725	GGACCGCATGTGGAGGGCCGGACACAGCTTGGCCGTGGCCGTGGCAAGTCAGCCT	784
Sbjct	502	GGACCGCATGTGGAGGGCCGGACACAGCTTGGCCGTGGCCGTGGCAAGTCAGCCT	561
Query	785	TCGCTATGATGGAGCACACCTCTGTGGGGATCCCTGCTCTCCGGGACTGGGTGCTGAC	844
Sbjct	562	TCGCTATGATGGAGCACACCTCTGTGGGGATCCCTGCTCTCCGGGACTGGGTGCTGAC	621
Query	845	AGCCGCCACTGCTTCCGGAGCGGAACCGGGCTGTCCGATGGCGAGTGGTGGCG	904

Sbjct	622	AGCCGCCCATTGCTCCCCGGAGCGGAACCGGGTCCCTGTCCGATGGCAGTGTGTCGG	681
Query	905	TGCCGTGCCAGGCCACTCCCCACGGCTCTGCAGCTGGGGTGCAGGCTGTGGTCTACCA	964
Sbjct	682	TGCCGTGCCAGGCCACTCCCCACGGCTCTGCAGCTGGGGTGCAGGCTGTGGTCTACCA	741
Query	965	CGGGGCTATCTTCCTTCGGGACCCAAACAGCGAGGAGAACAGAACGATATTGCCCT	1024
Sbjct	742	CGGGGCTATCTTCCTTCGGGACCCAAACAGCGAGGAGAACAGAACGATATTGCCCT	801
Query	1025	GGTCCACCTCTCCAGTCCCCCTGCCCTCACAGAAATACATCCAGCCTGTGCTCCCAGC	1084
Sbjct	802	GGTCCACCTCTCCAGTCCCCCTGCCCTCACAGAAATACATCCAGCCTGTGCTCCCAGC	861
Query	1085	TGCCGGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGCAACACGCA	1144
Sbjct	862	TGCCGGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGCAACACGCA	921
Query	1145	GTACTATGGCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGA	1204
Sbjct	922	GTACTATGGCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGA	981
Query	1205	TGTCTGCAATGGCGCTGACTTCTATGGAAACCAGATAAGCCAAAGATGTTCTGTGCTGG	1264
Sbjct	982	TGTCTGCAATGGCGCTGACTTCTATGGAAACCAGATAAGCCAAAGATGTTCTGTGCTGG	1041
Query	1265	CTACCCCGAGGGTGGCATGATGCCCTGCCAGGGCGACAGCGGTGGCCCTTGTGTTGA	1324
Sbjct	1042	CTACCCCGAGGGTGGCATGATGCCCTGCCAGGGCGACAGCGGTGGCCCTTGTGTTGA	1101
Query	1325	GGACAGCATCTCTGGACGCCACGGTGGCGCTGTGTGGCATTTGTGAGTTGGGCACTGG	1384
Sbjct	1102	GGACAGCATCTCTGGACGCCACGGTGGCGCTGTGTGGCATTTGTGAGTTGGGCACTGG	1161
Query	1385	CTGTGCCCTGGCCCAAAGCCAGGCCTACACCAAAGTCAGTGACTTCCGGAGTGGAT	1444
Sbjct	1162	CTGTGCCCTGGCCCAAAGCCAGGCCTACACCAAAGTCAGTGACTTCCGGAGTGGAT	1221
Query	1445	CTTCCAGGCCATAAAGACTCACTCGAAGCCAGCGGCATGGTGACCCAGCTCT	1497
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>gb|DQ892119.2| Synthetic construct clone IMAGE:100004749; FLH183205.01X; RZPDo839H04140D
hepsin (transmembrane protease, serine 1) (HPN)
gene, encodes complete protein
Length=1294

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]
(Over 10 PubMed links)

Score = 2309 bits (1250), Expect = 0.0
Identities = 1252/1253 (99%), Gaps = 0/1253 (0%)
Strand=Plus/Plus

Query	245	CATGGCGCAGAAGGAGGGTGGCCGGACTGTGCCATGCTGCTCCAGACCCAAGGTGGCAGC	304
Sbjct	22	CATGGCGCAGAAGGAGGGTGGCCGGACTGTGCCATGCTGCTCCAGACCCAAGGTGGCAGC	81
Query	305	TCTCACTGCGGGGACCTGCTACTTCTGACAGCCATCGGGCGGCATCCTGGGCATTGT	364
Sbjct	82	TCTCACTGCGGGGACCTGCTACTTCTGACAGCCATCGGGCGGCATCCTGGGCATTGT	141
Query	365	GGCTGTTCTCTCAGGAGTGACCAGGAGCCGTGTACCCAGTGCAGGTAGCTCTGCGGA	424
Sbjct	142	GGCTGTTCTCTCAGGAGTGACCAGGAGCCGTGTACCCAGTGCAGGTAGCTCTGCGGA	201
Query	425	CGCTCGGCTCATGGCTTGTACAAGACGGAAGGGACGTGGCGCTGTGTGCTCTCGCG	484
Sbjct	202	CGCTCGGCTCATGGCTTGTACAAGACGGAAGGGACGTGGCGCTGTGTGCTCTCGCG	261
Query	485	CTCCAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGATGGGCTTCTCAGGGCACTGAC	544
Sbjct	262	CTCCAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGATGGGCTTCTCAGGGCACTGAC	321
Query	545	CCACTCCGAGCTGGACGTGCGAACGGCGGGGCCAATGGCACGTCGGCTTCTCTGTGT	604
Sbjct	322	CCACTCCGAGCTGGACGTGCGAACGGCGGGGCCAATGGCACGTCGGCTTCTCTGTGT	381
Query	605	GGACGAGGGAGGCTGCCACCCAGAGGCTGTGGAGGTCACTCCGTGTGTGATTG	664
Sbjct	382	GGACGAGGGAGGCTGCCACCCAGAGGCTGTGGAGGTCACTCCGTGTGTGATTG	441
Query	665	CCCCAGAGGCCGTTCTGGCCGCATCTGCCAAGACTGTGGCCGCAGGAAGCTGCCGT	724
Sbjct	442	CCCCAGAGGCCGTTCTGGCCGCATCTGCCAAGACTGTGGCCGCAGGAAGCTGCCGT	501
Query	725	GGACCGCATGTGGAGGGCCGGACACCAAGCTTGGCCGTGGCCGTGGCAAGTCAGCCT	784
Sbjct	502	GGACCGCATGTGGAGGGCCGGACACCAAGCTTGGCCGTGGCCGTGGCAAGTCAGCCT	561
Query	785	TCGCTATGATGGAGCACACCTCTGTGGGGATCCCTGCTCTCCGGGACTGGGTGCTGAC	844
Sbjct	562	TCGCTATGATGGAGCACACCTCTGTGGGGATCCCTGCTCTCCGGGACTGGGTGCTGAC	621
Query	845	AGCCGCCACTGCTTCCGGAGCGGAACCGGGCTGTCCGATGGCAGTGTGCGG	904

Sbjct	622	AGCCGCCCATTGCTTCCCCGAGCGAACCGGGTCCGTCCGATGGCAGTGTTCGCGG	681
Query	905	TGCCGTGCCAGGCCACTCCCCACGGCTCGCAGCTGGGGTGCAGGCTGTGGTCTACCA	964
Sbjct	682	TGCCGTGCCAGGCCACTCCCCACGGCTCGCAGCTGGGGTGCAGGCTGTGGTCTACCA	741
Query	965	CGGGGGCTATCTTCCCTTCGGGACCCAAACAGCGAGGAACAGAACGATATTGCCCT	1024
Sbjct	742	CGGGGGCTATCTTCCCTTCGGGACCCAAACAGCGAGGAACAGAACGATATTGCCCT	801
Query	1025	GGTCCACCTCTCAGTCCCCTGCCCTCACAGAAATACATCCAGCCTGTGCTCCAGC	1084
Sbjct	802	GGTCCACCTCTCAGTCCCCTGCCCTCACAGAAATACATCCAGCCTGTGCTCCAGC	861
Query	1085	TGCCGGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGCAACAGCA	1144
Sbjct	862	TGCCGGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGCAACAGCA	921
Query	1145	GTACTATGGCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGA	1204
Sbjct	922	GTACTATGGCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGA	981
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Sbjct	982	TGTCTGCAATGGCGCTGACTTCTATGGAAACCAGATAAGCCAAAGATGTTCTGTGCTGG	1041
Query	1265	CTACCCCGAGGGTGGCATGGATGCCCTGCCAGGGCGACAGCGGTGGCCCTTGTGTGA	1324
Sbjct	1042	CTACCCCGAGGGTGGCATGGATGCCCTGCCAGGGCGACAGCGGTGGCCCTTGTGTGA	1101
Query	1325	GGACAGCATCTCTGGACGCCACGGTGGCGCTGTGTGGCATTTGTGAGTTGGGCACTGG	1384
Sbjct	1102	GGACAGCATCTCTGGACGCCACGGTGGCGCTGTGTGGCATTTGTGAGTTGGGCACTGG	1161
Query	1385	CTGTGCCCTGGCCCAGAAGCCAGGCCTACACCAAAGTCAGTGACTTCCGGAGTGGAT	1444
Sbjct	1162	CTGTGCCCTGGCCCAGAAGCCAGGCCTACACCAAAGTCAGTGACTTCCGGAGTGGAT	1221
Query	1445	CTTCCAGGCCATAAGACTCACTCGAAGCCAGCGGCATGGTGACCCAGCTCT	1497
Sbjct	1222	CTTCCAGGCCATAAGACTCACTCGAAGCCAGCGGCATGGTGACCCAGCTCT	1274

>gb|EU644753.1| Homo sapiens truncated hepsin serine protease mRNA, complete
cds
Length=1209

Score = 2228 bits (1206), Expect = 0.0
 Identities = 1206/1206 (100%), Gaps = 0/1206 (0%)
 Strand=Plus/Plus

Query	246	ATGGCGCAGAAGGAGGGTGGCCGACTGTGCCATGCTGCTCCAGACCCAAAGGTGGCAGCT	305
Sbjct	1	ATGGCGCAGAAGGAGGGTGGCCGACTGTGCCATGCTGCTCCAGACCCAAAGGTGGCAGCT	60
Query	306	CTCACTGCCGGGACCCCTGCTACTTCTGACAGCCATCGGGCGGCATCCTGGCATTGTG	365
Sbjct	61	CTCACTGCCGGGACCCCTGCTACTTCTGACAGCCATCGGGCGGCATCCTGGCATTGTG	120
Query	366	GCTGTTCTCTCAGGAGTGACCAGGAGCCGCTGTACCCAGTCAGCTCTGCGGAC	425
Sbjct	121	GCTGTTCTCTCAGGAGTGACCAGGAGCCGCTGTACCCAGTCAGCTCTGCGGAC	180
Query	426	GCTCGGCTCATGGCTTTGACAAGACCGAACGGGACGTGGCGCTGCTGTGCTCCTCGCGC	485
Sbjct	181	GCTCGGCTCATGGCTTTGACAAGACCGAACGGGACGTGGCGCTGCTGTGCTCCTCGCGC	240
Query	486	TCCAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGATGGCTTCTCAGGGACTGACC	545
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Query	546	CACTCCGAGCTGGACGTGCGAACGGCGGCCAATGGCACGTCGGCTTCTCTGTGTG	605
Sbjct	301	CACTCCGAGCTGGACGTGCGAACGGCGGCCAATGGCACGTCGGCTTCTCTGTGTG	360
Query	606	GACGAGGGGAGGCTGCCACACCCAGAGGCTGCTGGAGGTATCTCGTGTGATTG	665
Sbjct	361	GACGAGGGGAGGCTGCCACACCCAGAGGCTGCTGGAGGTATCTCGTGTGATTG	420
Query	666	CCCAGAGGCCGTTCTGGCCGCATCTGCCAAGACTGTGGCCGAGAACGCTGCCGTG	725
Sbjct	421	CCCAGAGGCCGTTCTGGCCGCATCTGCCAAGACTGTGGCCGAGAACGCTGCCGTG	480
Query	726	GACCGCATCGTGGAGGCCGGACACCAGCTGGCCGCGTGGCAAGTCAGCCTT	785
Sbjct	481	GACCGCATCGTGGAGGCCGGACACCAGCTGGCCGCGTGGCAAGTCAGCCTT	540
Query	786	CGCTATGATGGAGCACACCTCTGTGGGGATCCCTGCTCTCGGGACTGGGTGCTGACA	845
Sbjct	541	CGCTATGATGGAGCACACCTCTGTGGGGATCCCTGCTCTCGGGACTGGGTGCTGACA	600
Query	846	GCCGCCCACTGCTTCCCGAGCGAACCGGGTCTGTCCGATGGCAGTGTGCTGCCGT	905
Sbjct	601	GCCGCCCACTGCTTCCCGAGCGAACCGGGTCTGTCCGATGGCAGTGTGCTGCCGT	660
Query	906	GCCGTGGCCAGGCCCTCCCCACGGCTCTGCAGCTGGGGTGCAGGCTGTGGCTACCA	965

Sbjct	661	GCCGTGGCCCAGGCCCTCCCCACGGTCTGCAGCTGGGGTGCAGGCTGGTCTACCAC	720
Query	966	GGGGGCTATCTCCCTTTCGGGACCCCACAGCGAGGAGAACAGCAACGATATTGCCCTG	1025
Sbjct	721	GGGGGCTATCTCCCTTTCGGGACCCCACAGCGAGGAGAACAGCAACGATATTGCCCTG	780
Query	1026	GTCCACCTCTCCAGTCCCCCTGCCCTCACAGAATAACATCCAGCCTGGTGCCTCCAGCT	1085
Sbjct	781	GTCCACCTCTCCAGTCCCCCTGCCCTCACAGAATAACATCCAGCCTGGTGCCTCCAGCT	840
Query	1086	GCCGGCCAGGCCCTGGTGATGGCAAGATCTGTACCGTGACGGGCTGGGCAACACCGAG	1145
Sbjct	841	GCCGGCCAGGCCCTGGTGATGGCAAGATCTGTACCGTGACGGGCTGGGCAACACCGAG	900
Query	1146	TACTATGGCCAACAGGGGGGACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGAT	1205
Sbjct	901	TACTATGGCCAACAGGGGGGACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGAT	960
Query	1206	GTCTGCAATGGCGCTGACTTCTATGGAAACAGATCAAGCCCAAGATGTTCTGTGCTGGC	1265
Sbjct	961	GTCTGCAATGGCGCTGACTTCTATGGAAACAGATCAAGCCCAAGATGTTCTGTGCTGGC	1020
Query	1266	TACCCCGAGGGTGGATTGATGCCCTGCCAGGGCGACAGCGGTGGTCCCTTGTGTGAG	1325
Sbjct	1021	TACCCCGAGGGTGGATTGATGCCCTGCCAGGGCGACAGCGGTGGTCCCTTGTGTGAG	1080
Query	1326	GACAGCATCTCTGGACGCCACGGTGGCGCTGTGGCATTGTGAGTTGGGGCACTGGC	1385
Sbjct	1081	GACAGCATCTCTGGACGCCACGGTGGCGCTGTGGCATTGTGAGTTGGGGCACTGGC	1140
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>emb|X07002.1|HSHEPSL H.sapiens liver mRNA for serine protease hepsin
Length=1199

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]
(Over 10 PubMed links)

Score = 2215 bits (1199), Expect = 0.0
Identities = 1199/1199 (100%), Gaps = 0/1199 (0%)
Strand=Plus/Plus

Query	585	ACGTCGGGCTTCTTCTGTGTGGACGAGGGAGGCTGCCACACCCAGAGGCTGGAG	644
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Query	645	GTCATCTCCGTGTGATGCCAGAGGGCGTTCTTGGCGCATCGCAAGACTGT	704
Sbjct	61	GTCATCTCCGTGTGATGCCAGAGGGCGTTCTTGGCGCATCGCAAGACTGT	120
Query	705	GGCCGCAGGAAGCTGCCGTGGACCGCATCGTGGGAGGCGGGACACCAGCTGGCGG	764
Sbjct	121	GGCCGCAGGAAGCTGCCGTGGACCGCATCGTGGGAGGCGGGACACCAGCTGGCGG	180
Query	765	TGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGGATCCCTGCTC	824
Sbjct	181	TGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGGATCCCTGCTC	240
Query	825	TCCGGGGACTGGGTGCTGACAGCGCCCACTGCTCCGGAGCGGAACCGGGTCCGTCC	884
Sbjct	241	TCCGGGGACTGGGTGCTGACAGCGCCCACTGCTCCGGAGCGGAACCGGGTCCGTCC	300
Query	885	CGATGGCGAGTGTGTTGCCGTGCCAGGCCCTCTCCCCACGGCTGCAGCTGGGG	944
Sbjct	301	CGATGGCGAGTGTGTTGCCGTGCCAGGCCCTCTCCCCACGGCTGCAGCTGGGG	360
Query	945	GTGCAGGCTGTGGTCTACACAGGGGCTATCTCCCTTCTGGGACCCAAACAGCGAGGAG	1004
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Sbjct	421	AACAGCAACGATATTGCCCTGGTCCACCTCTCCAGTCCCTGCCCTCACAGAAATACATC	480
Query	1065	CAGCCTGTGCCTCCAGCTGCCGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTG	1124
Sbjct	481	CAGCCTGTGCCTCCAGCTGCCGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTG	540
Query	1125	ACGGGCTGGGCAACACGCAGTACTATGCCAACAGGCCGGGTACTCCAGGAGGCTCGA	1184
Sbjct	541	ACGGGCTGGGCAACACGCAGTACTATGCCAACAGGCCGGGTACTCCAGGAGGCTCGA	600
Query	1185	GTCCCCATAATCAGCAATGATGTCTGCAGTGGCGCTGACTTCTATGAAACAGATCAAG	1244
Sbjct	601	GTCCCCATAATCAGCAATGATGTCTGCAGTGGCGCTGACTTCTATGAAACAGATCAAG	660
Query	1245	CCCAAGATGTTCTGTGCTGGCTACCCCGAGGGTGGCATTGATGCCCTGCCAGGGCACAGC	1304
Sbjct	661	CCCAAGATGTTCTGTGCTGGCTACCCCGAGGGTGGCATTGATGCCCTGCCAGGGCACAGC	720

Query	1305	GGTGGTCCCTTGTGTGAGGACAGCATTCTCGGACGCCACGTTGGCGGCTGTGTGGC	1364
Sbjct	721	GGTGGTCCCTTGTGTGAGGACAGCATTCTCGGACGCCACGTTGGCGGCTGTGTGGC	780
Query	1365	ATTGTGAGTTGGGGCACTGGCTGTGCCCTGGCCAGAACGCCAGGCCTACACCAAAGTC	1424
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Query	1425	AGTGACTTCGGGAGTGGATCTTCAGGCCATAAAGACTCACTCCGAAGCCAGGGCATG	1484
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Sbjct	901	GTGACCCAGCTCTGACCGGTGGCTTCGCTGCGCAGGCCCTCAGGGCCGAGGTGATCCC	960
Query	1545	GGTGGTGGATCCACGCTGGCCAGGATGGGACGTTTTCTTCTGGCCCGGTCCACA	1604
Sbjct	961	GGTGGTGGATCCACGCTGGCCAGGATGGGACGTTTTCTTCTGGCCCGGTCCACA	1020
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Sbjct	1021	GGTCCAAGGACACCCCTCCCTCCAGGGTCTCTCTTACAGTGGGGCCACTCAGCCC	1080
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Sbjct	1081	CGAGACCACCCAAACCTCACCCCTCTGACCCCCATGTAAATATTGTTCTGCTGTGGGAC	1140
Query	1725	TCTGTCTAGGTGCCCTGATGATGGGATGCTTTAAATAATAAAAGATGGTTTGATT	1783
Sbjct	1141	TCTGTCTAGGTGCCCTGATGATGGGATGCTTTAAATAATAAAAGATGGTTTGATT	1199

>dbj|AK233353.1| Sus scrofa mRNA, clone:LVRM10127D02, expressed in liver
Length=1785

Score = 2069 bits (1120), Expect = 0.0
Identities = 1547/1750 (88%), Gaps = 42/1750 (2%)
Strand=Plus/Plus

Query	66	CCACGCCACCGCCTCTGCCCTCC-AGGCCGCCGCTGCTGGGGGCCACCATGCTCCCTGCC	124
Sbjct	21	CCAC-CCGCTGCCCTCTGCCCTCCGGGGCC-TCCGCCGCTGCCGGGCCACCGTGCTCCCTGCC	78
Query	125	CAGGCCTGGAGACTGA-CCC-GACCCCCGCA-C-TACCTCGAGGCTCCGGCCCCACCTGC	180
Sbjct	79	CAGGCCTGGAGACTGACCCCTAAAACCCGCACCGTGTCTC-A-GCTCTGCCCTACCCGC	136
Query	181	TGGACCCAGGGTCCCACCTGGCCCAGGAGGTCAAGCCAGGGATCATTAACAAGAGGCA	240
Sbjct	137	CGGACCCAGGGTCCCAGGGCCAGGAGGTCAAGCCGGGGATCATTAACTAGAGGCC	196
Query	241	GTGACATGGCCAGAAGGAGGGTGGCCGACTGTGCATGCTGCTTAGCCAGACCCAAAGTGG	300
Sbjct	197	GTGACATGGCCAGAAGGAGGGTGGCCAGGCTGTCTAGCTGCTCCGGACCCAAAGTGG	256
Query	301	CAGCTCTCACTGCCGGGACCCCTGCTACTCTGACAGCCATGGGGCGGATCCTGGGCA	360
Sbjct	257	CAGCTCTCACTGTGGGACCGTGTCTGCTGACAGGCATTGGGCCAGGGCTGGGCA	316
Query	361	TTGTGGCTTTCTCTCAGGAGTGACCAAGGGCTGTACCCAGTCAGGTCACTCTG	420
Sbjct	317	TTGTGACCGTTACTCAGGAGTGACCAAGGGCTGTATCCAGTCAGGTGGGGCC	376
Query	421	CGGACGCTGGCTATGGCTTTGACAAGACGGAAGGG-ACGTGGGGCTGCTGTCTCC	479
Sbjct	377	GGGATTCTGGCTACCGTGTTGAGACGG-AGGCACGTGGGCCTGCTGTCTCC	435
Query	480	TCGCGCTCAAACGCCAGGGTAGCCGACTCAGCTGCCAGGAGATGGCTTCTCAGGGCA	539
Sbjct	436	TCGCGCTCAAACGCCAGGGTAGCCGACTCAGCTGCCAGGAGATGGCTTCTCAGGTCA	495
Query	540	CTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGGCCAATGGCACGTGGCTTCTTC	599
Sbjct	496	CTGACCCACTCAGAGCTGGATGTGCCACTGCCGGGCCAACGGCACGTGGCTTCTTC	555
Query	600	TGTGTGGACGAGGGAGGTGCCCCACACCCAGAGGTGCTGGAGGTATCTCCGTGTG	659
Sbjct	556	TGTGTGGATGAGGGAGGTGCGCAGGCCGGAGGTGCTTGAGGTCTCTGTGTGC	615
Query	660	GATTGCCCAAGAGGCCATTCTGGCCGCATC-TGCCAAGACTGTGGCCGCAGGAAGCT	718
Sbjct	616	GACTGTCCCAGGGCCATTCTGGCAACCA-CATGCCAAGACTGCCGCATAGGAAGCT	674
Query	719	GCCCCTGGACCGCATCGTGGAGGCCGGACACCAAGCTTGGCCGGTGGCCGTGGCAAGT	778
Sbjct	675	GCCCCTGGATCGCATGGCCGGTCAAGGACACCAGGCTGGCCGGTGGCCGTGGCAAGT	734
Query	779	CAGCCTTCGCTATGATGGAGCACACCTCTGTGGGGATCCCTGCTCTGGGGACTGGGT	838
Sbjct	735	CAGTCTTCGCTACGACGGAGCACACCTCTGTGGGGATCCCTGCTCTCAAAGACTGGGT	794
Query	839	GCTGACAGCCGCCACTGCTTCCGGAGCGGAACCGGGCTGTCCGATGGCGAGTGT	898
Sbjct	795	GCTGACAGCCGCCACTGCTTCCCGAGCGGAACCGGGCTGTCTCGATGGCGAGTATT	854
Query	899	TGCCGGTGCCGTGGCCAGGCCTCTCCCCACGGCTGCACTGGGTGCAGCTGGGT	958

Sbjct	855	CGCCGGTGCCTGTGGCCCAGACCTCACCCCACGGCCTGAGATGGGGTGAGCGCGGTGAT	914
Query	959	CTACCACGGGGCTATCTCCCTTTCGGGACCCAAACAGCGAGGAGAACAGCAACGATAT	1018
Sbjct	915	CTACCATGGGACTATCTCCCTTTCGAGACCCAAACAGTGAGGAGAACAGCAATGATAT	974
Query	1019	TGCCCTGGTCCACCTCTCAG-TCCCTGCCCTCACAGAATACATCCAGCTGTGCCCC	1077
Sbjct	975	CGCCCTGGTCCACCTCTCAGCTCCC-TGGCTCTCACAGAATACATCCAGCTGTGCCCC	1033
Query	1078	TCCCAGCTGCCGGCAGGGCCCTGGTGGATGGCAAGATCTGTACCGTGAGGGCTGGGCA	1137
Sbjct	1034	TCCCAGCTGCCGGCAGGGCCCTGGTGGACGGCAAGATCTGCACGGTGACAGGCTGGGCA	1093
Query	1138	ACACGCAGTAATGGCCAACAGGCCGGGACTCCAGGAGGCTCGAGTCCCCATAATCA	1197
Sbjct	1094	ACACGCAGTAATACGGCCAACAGGCTGGGTGCTCACAGGAGGCCAGTCCCCATAATCA	1153
Query	1198	GCAATGATGCTGCAATGGCGCTGACTTCTATGGAAACAGATCAAGCCAAAGATGTTCT	1257
Sbjct	1154	GCAATGATGCTGCAATGCCCGGACTTCTACGGAAACAGATCAAGCCAAAGATGTTCT	1213
Query	1258	GTGCTGGCTACCCCGAGGGTGGCATTGATGCCCTGCCAGGGCAGCGGTGGTCCCTTG	1317
Sbjct	1214	GTGCCGGCTACCCCTGAGGGTGGCATTGACGCCCTGCCAGGGTGACAGTGGTGGCCCTTCG	1273
Query	1318	TGTGTGAGGACAGCATCTCGGACGCCACGTTGGCGCTGTGTGGATTGTGAGTTGGG	1377
Sbjct	1274	TGTGTGAGGACAGCATCTCGGACGCCACGTTGGCGCTGTGTGGCATCGTGAGCTGGG	1333
Query	1378	GCACTGGCTGTGCCCTGGCCCAAAGGCCAGGCCTACACCAAAGTCAGTGACTTCCGGG	1437
Sbjct	1334	GCACCCGGCTGTGCCCTGGCCCAAAGGCCAGGCCTACACCAAAGTCAGTGACTTCCGGG	1393
Query	1438	AGTGGATCTCCAGGCCATAAAGACTCACTCCGAAGCCAGGGCATGGTGACCCAGCTCT	1497
Sbjct	1394	AGTGGATCTCCAGGCCATAAAGACTCACTCCGAAGCCAGGGCATGGTGACCCAGCTCT	1453
Query	1498	GACCGGTGGCTTCT-C-GCTGCGCA-GCCTCCAGGGCCCAGGTGATCCGGTGG-TG-	1551
Sbjct	1454	GACCTGCGGCTTCTGCTGCGCTGCCCTCAGGGCCAAGCTGATCCAGGTGGCTCC	1513
Query	1552	-G-----GATC-----CACGCTGGGCC-GAGGAATGGGACGTTTTCTTCTTGGGCC	1596
Sbjct	1514	AGCCCCCTCATGATGGGTTCACCCCTGGGCTG-GGATAGAACATTCTTCTTGGGCC	1572
Query	1597	GGTCCACAGGTCAAAGGACACCCCTCCAGGGTCTCTCTTCCACAGTGCGGGCCCA	1656
Sbjct	1573	AGCCCCACAGGTCCAAGGATACCCCTCCCAAGGTCTCTCTTCCACAGTGCGGGCCCA	1632
Query	1657	CTCAGCCCCGAG-ACCACCAA-CCTCACCCCTCTGACCCCCATGTAATATTGTTCTGC	1714
Sbjct	1633	CTCAGGCCCTG-GCATCACCGAGCCTCACCCCTCTGACCCCCATGTAATATTGTTCTGC	1691
Query	1715	TGTCTGGGA-CTCCTGTCTAGGTGCCCTGATGATGGGATGCTTTAAATAAAAGAT	1773
Sbjct	1692	CATCTGGGGCCCTATCTAG-TGCCCTGATGACAGGATGCTTTAAATAAAAGAT	1750
Query	1774	GGTTTTGATT 1783	
Sbjct	1751	GGTTTTGATT 1760	

>ref|NM_001080241.2| Bos taurus hepsin (transmembrane protease, serine 1) (HPN), mRNA
 gb|BC140636.1| Bos taurus hepsin (transmembrane protease, serine 1), mRNA (cDNA clone MGC:148484 IMAGE:8196479), complete cds
 Length=1919

GENE ID: 508148 HPN | hepsin (transmembrane protease, serine 1) [Bos taurus]
 (10 or fewer PubMed links)

Score = 1973 bits (1068), Expect = 0.0
 Identities = 1552/1777 (87%), Gaps = 67/1777 (3%)
 Strand=Plus/Plus

Query	49	GCCTGGCTTAGCAGGCCAACGC-CA-CCGC--C-TCTGCCTCCAGGCC-GCCCCCTGCT	102
Sbjct	2	GCCAGGCTTAGCAGGCCCTCGCGCTGCCCTGCCCT-GGCCCTGCCGCT	60
Query	103	GCGGGGCCACCATGCTCTGCCAGGCCAGGTGGAGACTGACCCGAC-CCCGGACTA-C-CT	159
Sbjct	61	GCGGGGCCACCATGCTCTGCCAGGCCAGGTGGAGACTGACCCCTAAACCG-CACCATCTCT	119
Query	160	CGAGGCTCGCCCCCACCTGCTGGACCCCAAGGGTCCACCCCTGGCCAGGGAGGTAGCCA	219
Sbjct	120	C-AG-CTCCGCCCCCACCTGCGGACCCCAAGGGTCCCGCCCCGGGGAGGTAGCCA	177
Query	220	GGGAATCATTAACAAGAGGCAGTGACATGGGCCAGAAGGAGGGTGCCGGACTGTGCCAT	279
Sbjct	178	GGGAATCATTAACTAGAGGCTGTGACATGGGCCAGAAGGAGGGTGCCGGACTGTGCCAT	237
Query	280	GCTGCTCCAGACCCAAAGGTGGCAGCTCTCACTGCGGGGACCTGCTACTTCTGACAGCCA	339
Sbjct	238	GCTGCTCCGACCCAAAGGTGGCCCTCTCACTGTTGGGACCTGCTCTGACAGGCA	297
Query	340	TCGGGGCGGACCTGGGCCATTGTGGCTGTTCTCTCAGGAGTGACAGGAGGCCGCTGT	399

Sbjct	298	TCGGGGCAGCGCTCTGGGCATTGTA CTGTTCTACTCAGGAGTGA TCAGGAGCCACTGT	357
Query	400	ACCCAGTGCAGGTCAGCTCTGCGACGCTCGGCTCATGGCTTTGACAAGACGGAAGGG-	458
Sbjct	358	ATCCAGTGCAGGTCAGGCCCGGCCGATGCTCGGCTCACGGTGTGACCCAGACAGA-GGGC	416
Query	459	ACGTGGCGCTGCTGTGCTCTCGCGCTCCAAACGCCAGGGTAGCCGGACTCAGCTCGAG	518
Sbjct	417	ACGTGGCGCTGCTTTGCTCTCGCGCTCCAATGCCAGGGTGGCGGGCTCAGCTCGAG	476
Query	519	GAGATGGGCTTCCTCAGGGCACTG-ACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGC	577
Sbjct	477	GAGATGGGCTTCCTCAGGGCGTTGGACTT-CTCGGAGCTGGACGTGCGAACGGCGGGCGC	535
Query	578	CAATGGCACGTCGGCTTCTTCTGTGGACGAGGGGAGGCTGCCCAACCCAGAGGCT	637
Sbjct	536	CAATGGCACGTCGGCTTCTTCTGCGTGGACGAGGGGAGGCTGCCCATGCCGAGGTT	595
Query	638	GCTGGAGGTCACTCCGTGTGATTGCCCAAGAGGGCGTTCTGGCCGCATCTGCCA	697
Sbjct	596	GCTCGAGGCTCCTCTCGTGTGCGACTGTCCAGAGGGCGTTCTGGCTACCAGCTGCCA	655
Query	698	AGACTGTGGCCGCAGGAAGCTGCCGTGGACCGCATCGTGGAGGGCGGGACACCAGCTT	757
Sbjct	656	AGACTGTGGCCACCGAAAACCGATCGCGTGTGCGATCGCATTGTCGGCGCCAGGACACCAGCCT	715
Query	758	GGGCCGGTGGCGTGGCAAGTCAGCCTCGCTATGATGGAGCACACCTCTGTGGGGATC	817
Sbjct	716	GGGCAGGTGGCGTGGCAAGTCAGTCTCGCTATGATGGAGCACATCTGTGGGGGTC	775
Query	818	CCTGCTCTCGGGGACTGGGTGCTGACAGCCGCCACTGCTTCCGGAGCGGAACCGGGT	877
Sbjct	776	CGTGCTCTCTAGGGACTGGGTGCTGACAGCCGCCACTGCTTCCCTGAGCGGAACCGGGT	835
Query	878	CCTGTCGGGATGGCAGTGTGTTGCGGTGCGTGGCCAGGGCTCTCCCACGGTC-TGC	936
Sbjct	836	CCTATCACGATGGCAGTGTGTTGCTGGCTGTGGCCAGACTTCACCCATGG-CGTGC	894
Query	937	AGCTGGGGTGCAGGCTGTTCTACACGGGGCTATCTCCCTTCGGGACCCAAACA	996
Sbjct	895	AACTGGGGTGCAGGCTGTCACTACCATGGGGCTATCTCCCTTCGGGAGACCCAAACA	954
Query	997	GCGAGGAGAACAGCAACGATATTGCCCTGGTCACCTCTCCAGTC-CCCTGCCCTCACA	1055
Sbjct	955	GCGAGGAGAATAGCAATGACATGCCCTGGTCCACCTCTCCGG-CACCTGCCCTCACA	1013
Query	1056	GAATACATCAGCCCTGTGTCGCTCCAGCTGCCGGCAGGGCTGGTGTGATGGCAAGATC	1115
Sbjct	1014	GAGTACATCAGCCCGTGTGTCCTCCGGCTGCCGGCAGGGCTGGTGTGATGGCAAGATC	1073
Query	1116	TGTACCGTGACGGCTGGGCAACACGCACTATGGCAACAGGCCGGGTACTCCAG	1175
Sbjct	1074	TGCACGGTGA CTGGCTGGGCAACACGCACTACAGGCCAACAGGCTGGGTGCTCCAG	1133
Query	1176	GAGGCTCGAGTCCCCATAATCAGCAATGATGTCGCAATGGCGTGA CTTCTATGGAAAC	1235
Sbjct	1134	GAGGCCCGAGTCCCCATAATCAGCAATGATGTCGCAACGCCCGACTTCTACGGGAAC	1193
Query	1236	CAGATCAAGCCCAAGATGTTCTGCTGGCTACCCCGAGGGTGGCATTTGATGCCCTGCCAG	1295
Sbjct	1194	CAGATCAAGCCCAAGATGTTCTGCTGGCTACCCCTGAGGGTGGCATTTGATGCCCTGCCAG	1253
Query	1296	GGCGACAGCGGTGGCTCCCTTGTGTA GAGGACAGCATCTCTCGGACGCCACGTTGGCGG	1355
Sbjct	1254	GGCGACAGTGGTGGCCCTTCTGCTGTGAGGATAGCATCTCTCGGACGCCACGTTGGCGG	1313
Query	1356	CTGTGTGGCATTGTA GAGTTGGGCACTGGCTGTG CCCTGGCCAGAACGCCAGGGCTTAC	1415
Sbjct	1314	CTGTGTGGCATTGTA GAGCTGGGCACTGGCTGTG CCCTGGCCAGAACGCCAGGGCTTAC	1373
Query	1416	ACCAAAAGTCAGTGACTTCGGGAGTGGATCTTCAGGCCATAAAAGACTCACTCCGAAAGCC	1475
Sbjct	1374	ACCAAAAGTCAGTGACTTCGGGAGTGGATCTTCAGGCCATAAAAGACTCACTCCGAAAGCC	1433
Query	1476	AGCGGCATGGTGCAGCCAGCTCTGACCGGTGGCTTC- GTCGCCA-GCCTCCAGGGC	1531
Sbjct	1434	AGCGGCATGGTAACCCAGTTGACCTGTGGCTTCTCCCTGCTGTGCAACGCCAGGGC	1493
Query	1532	CCGAGGTGATC-----CC----G-----GTGGTGGGATCCACGCTGGGCCAGG-ATG	1574
Sbjct	1494	CCGAGCTGATCTAAGGGGCCAGGCCACGCTGATGGGTTCACCTGGGCC-AGGGATG	1552
Query	1575	GGACGTTTCTTCTTCTGGGCCCGTCCACAGGTTCAAGGACACCCCT-CCCTCCAGGGTCC	1633
Sbjct	1553	GAACATTTTCTTCTTCTGGGCCAGGCCACAGGTTCAAGGATACTCTCCCTCCAAGGTCC	1612
Query	1634	TCTCTTCCACAGTGGCGGCCACTCAGCCCCAGACCCACCCACCTCACCCTCTGACC	1693
Sbjct	1613	TC-C----ACAGTGGCGGCCACTCAGCCCCAGACCCACCCACCTCACCCTCTGACC	1657
Query	1694	CCCATGTAAATATTGTTCTGCTGTGGGA-CTCTG-----TCTAGGTGCCCTGATG	1746
Sbjct	1658	CCCATGTAAATATTGTTCTGCTGTGGGA-CTCTG-----TCTAGGTGCCCTGATG	1716
Query	1747	ATGGGATGCTCTTAAATAATAAAAGATGGTTTGATT	1783
Sbjct	1717	ACAGGATGCTCTTAAATAATAAAAGATGGTTTGATT	1753

>gb|BT029913.1| Bos taurus hepsin (transmembrane protease, serine 1) (HPN), mRNA, complete cds
Length=1704

GENE ID: 508148 HPN | hepsin (transmembrane protease, serine 1) [Bos taurus]
(10 or fewer PubMed links)

Score = 1956 bits (1059), Expect = 0.0
Identities = 1514/1727 (87%), Gaps = 58/1727 (3%)
Strand=Plus/Plus

Query 91	CCGCCCCGCTGCTGCGGGGCCACCATGCTCCTGCCAGGCCCTGGAGACTGACCC-GACCC	149
Sbjct 2	CCGCCTGCTGCTGCGGGGCCACCATGCTCCTGCCAGGCCCTGGAGACTGACCC-TAAACCC	61
Query 150	GGCACTA-C-CTCGAGGCTCCGCCACCTGCTGGACCCAGGGTCCCACCCCTGGCCCA	207
Sbjct 62	-GCACCATCTCTC-A-GCTCCGCCACCTGCCGGACCCAGGGTCCCAGCCGGCCCC	118
Query 208	GGAGGTCAAGCAGGAAATCATTAAACAAGAGGCAGTGACATGGCGCAGAAGGAGGGTGGCC	267
Sbjct 119	GGAGGTCAAGCAGGAAATCATTAACTAGAGGCTGTGACATGGCGAGAAGGAGGGTGGCC	178
Query 268	GGACTGTGCCATGCTGCCAGACCCAAAGGTGGCAGCTCTCACTGCCGGGACCCCTGCTAC	327
Sbjct 179	GGACTGTGCCATGCTGCCAGACCCAAAGGTGGCAGCTCTCACTGTGGGGACCGTCTGC	238
Query 328	TTCTGA CAGCCATCGGGCGGCATCCTGGGCATTGTGGCTGTTCTCCTCAGGAGTGACC	387
Sbjct 239	TCCCTGA CAGGCATCGGGCAGCGCTCTGGGCATTGTGACTGTTCTACTCAGGAGTGATC	298
Query 388	AGGAGCCGCTGTACCCAGTGCAGGTCTGCCAGCTCGGGCTATGGTCTTGACA	447
Sbjct 299	AGGAGGCCACTGTATCCAGTGCAGGTGCCCGCGGGATGCTCGGCTCACGGTGTGACC	358
Query 448	AGACGGAAGGG-ACGTGGCGCTGCTGTGCTCCTCGCCTCCAACGCCAGGGTAGCCGA	506
Sbjct 359	AGACAGA-GGGCACGTGGCGCTGCTTGTCTCGCCTCCAATGCCAGGGTGGCGGG	417
Query 507	CTCAGCTGCGAGGAGATGGGCTTCCTCAGGGCACTG-ACCCACTCCGAGCTGGACGTGCG	565
Sbjct 418	CTCAGCTGCGAGGAGATGGGCTTCCTCAGGGCGTTGACTT-CTCGGAGCTGGACGTGCG	476
Query 566	AACGGCGGGCGCAATGCCACGTGGCTGGCTTCTCTGTGTGGACGAGGGAGGCTGCCCA	625
Sbjct 477	GACGGCAGGGCGCAATGCCACGTGGCTGGCTTCTCTGTGTGGACGAGGGAGGCTGCCGA	536
Query 626	CACCCAGAGGCTGCTGGAGGTATCTCGTGTGTGATTGCCAGAGGCCGTTCTTGGC	685
Sbjct 537	TGCCCCGGAGGTGCTCGAGGTCTCTCGTGTGCGACTGTCCCAGAGGCCGTTCTTGGC	596
Query 686	CGCCATCGCCAAGACTGTGGCCGCAGGAAGCTGCCGTGGACCGCATCGGGAGGCCG	745
Sbjct 597	TACCACTGCCAACGAACTGTGGCCACCGAAAATGCCGGTCGATCGCATTGTGGCGCCA	656
Query 746	GGACACCAAGCTGGGCCGGTGGCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCT	805
Sbjct 657	GGACACCAAGCTGGCCAGGTGGCGTGGCAAGTCAGCTTCGCTATGATGGAGCACATCT	716
Query 806	CTGTGGGGATCCCTGCTCTCGGGGACTGGGTGCTGACAGCCGCCACTGCTTCCCGA	865
Sbjct 717	CTGTGGGGGTCCGTGCTCTAGGGACTGGGTGCTGACAGCCGCCACTGCTTCCCTGA	776
Query 866	GCGGAACGGGTCTGCTCCGATGGCGAGTGTGTTGCCGGTGCCGGCTCCAGGCCCTCC	925
Sbjct 777	GCGGAACGGGTCTATCACGATGGCGAGTGTGTTGCTGGTGCTGGCCAGACTTCACC	836
Query 926	CCACGGTC-TGCAGCTGGGGTGCAGGTGTGGCTACACAGGGGCTATCTCCCTTC	984
Sbjct 837	CCATGG-CGTGCAACTGGGGTGCAGGTGTACATACAGGGGCTATCTCCCTTC	895
Query 985	GGGACCCCAAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCACCTCTCCAGTC-CC	1043
Sbjct 896	GAGACCCCAAACAGCGAGGAGAACAGCAATGACATGCCCTGGTCCACCTCTCCGG-CACC	954
Query 1044	CTGCCCTCACAGAAATACATCCAGCTGTGTGCTCCAGCTGCCGGCAGGCCCTGGT	1103
Sbjct 955	CTGCCCTCACAGAACTACATCCAGCCGTGTGTCTCCCGCTGCCGGCAGGCCCTGGT	1014
Query 1104	GATGGCAAGATCTGTACCGTGACGGCTGGGCAACACGCAGTACTATGGCAACAGGCC	1163
Sbjct 1015	GATGGCAAGATCTGCACGGTGACTGGCTGGGCAACACGCAGTACTACGCCAACAGGCT	1074
Query 1164	GGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAATGGCGCTGAC	1223
Sbjct 1075	GGGGTGTCCAGGAGGCCAGTCCCCATAATCAGCAATGATGTCTGCAACGCCCGAC	1134
Query 1224	TTCTATGAAACCAAGATCAAGGCCAAGATGTTCTGTGTGCTGGCTACCCGAGGGTGGCATT	1283
Sbjct 1135	TTCTACGGAAACCAAGATCAAGGCCAAGATGTTCTGTGTGCTGGCTACCCGAGGGTGGCATT	1194
Query 1284	GATGCCCTGCCAGGGCGACAGCGGTGGTCCCTTGTGTGAGGACAGCATCTCGGACG	1343
Sbjct 1195	GATGCCCTGCCAGGGCGACAGCGGTGGCCTTCGTGTGAGGATAGCATCTCGGACG	1254

Query	1344	CCACGTTGGCGGGCTGTGGCATTGTGAGTTGGGCACTGGCTGTGCCCTGGCCAGAACG	1403
Sbjct	1255	CCACGTTGGCGGGCTGTGGCATTGTGAGTTGGGCACCGGCTGTGCCCTGGCCAGAACG	1314
Query	1404	CCAGGGCTACACCAAAGTCAGTGACTTCCGGAGTGGATCTTCAGGCCATAAAGACT	1463
Sbjct	1315	CCAGGGCTACACCAAAGTCAGTGACTTCCGGAGTGGATCTTCAGGCCATAAAGACT	1374
Query	1464	CACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTCTCTC---GCTGCGCA	1520
Sbjct	1375	CACTCCGAAGCCAGCGGCATGGTAACCCAGCTTGAACCTGTGGCTCTCTCGCTGTGCA	1434
Query	1521	-GCCTCCAGGGCCCAGGGTGATC-----CC---G-----GTGGTGGGATCCACGCTG	1563
Sbjct	1435	CGCCTCCAGGGCCCAGGTGATCTAAGGGGCCACGGCCACGTGATGGGTTCACCTG	1494
Query	1564	GGCCGAGG-ATGGGACGTTTTCTTCTGGGCCGGTCCACAGGTTCAAGGACACCC-C	1621
Sbjct	1495	GGCC-AGGGATGAAACATTTCCTTCTGGGCCAGGCCACAGGTTCAAGGATACTCTTC	1553
Query	1622	CCTCCAGGGCTCTCTTCAACAGTGGCGGGCCACTCAGCCCCGAGACCACCAACCTC	1681
Sbjct	1554	CCTCCAAAGGTCTCTC---C---ACAGTGGCGGGCCACTCAGCCCTGGGACCCACCC---TC	1604
Query	1682	ACCCCTCTGACCCCCATGTAATATTGTTCTGCTGTGGACTCCTG----TCTAGGT	1736
Sbjct	1605	-C---TGC---CCCCATGTAATATTGTTCTGCCATCTGGGACCCCCCCCCCATCTTG-T	1657
Query	1737	GCCCCTGATGATGGGATGCTTTAAATAAAAGATGGTTTGATT	1783
Sbjct	1658	GCTCCTGAAGACAGGATGCTTTAAATAAAAGATGGTTTGATT	1704

>ref|XM_541697.2| PREDICTED: Canis familiaris similar to Serine protease hepsin (Transmembrane protease, serine 1) (LOC484583), mRNA Length=1460

GENE ID: 484583 HPN | hepsin (transmembrane protease, serine 1)
[Canis lupus familiaris]

Score = 1873 bits (1014), Expect = 0.0
Identities = 1322/1470 (89%), Gaps = 24/1470 (1%)
Strand=Plus/Plus

Query	75	CGCCTCTGCCCTCAGGCCGCCGCTGCTGCGGGGCCACCATGCTCTGCCAGGGCTGGA	134
Sbjct	1	CGCCTCTGCCCTCCGGCC-ACCGC-C-GCGGGGCCACCATGCTCCGCCAGGGCTGGA	56
Query	135	GACTGACCC-GACCCCGGCACTACCTCGAGGCTCCGCCACCTGCTGGACCCAGGGT	193
Sbjct	57	GACTGACCCGGA-GAGGGCACTATCTC-A-GCTCCGCCACCTGCGGACCCAGGGT	113
Query	194	CCCACCCCTGGCCCAGGAGTCAGCCAGGGAACTATTAAACAGAGGCACTGACATGGGCA	253
Sbjct	114	CCCACCCCGGCCGGAGGTCAAGCCAGGGAACTATTAAACAGAGGCGTGACATGGGGA	173
Query	254	GAAGGAGGGTGGCCGGACTGTGCATGCTGCTCCAGACCCAAGGGTGGCAGCTCTCACTGC	313
Sbjct	174	GAAGGAGGGTGGCCGGACTGTGCATGCTGTTCCGGACCCAAGGGTGGCAGCTCTCACTGC	233
Query	314	GGGGACCCCTGCTACTTCTGACAGCCATGGGGCGGCATCTGGGCATTGTG-GCTGTT	372
Sbjct	234	AGGGACCCCTGCTGCTCTGACAGGCATGGGGCAGCGTCTGGGCATTGTGACCT-TCC	292
Query	373	TCCTCAGGAGTGACCAAGGAGCGCTGTACCCAGTGCAGGTCAGCTCTGGAC-GCTCGG	431
Sbjct	293	TACTCAAGAGTGTACAGGAGCGCTGTATCGGTGCAGGCCAGCCCTGCCAGGG-CGG	351
Query	432	CTCATGGTCTTGACAAGACGGAAGGG-ACGTGGCGCTGCTGTGCTCTCGCGCTCAA	490
Sbjct	352	CTCATGGTGGTTCGAGACACGG-AGGGCACGTGGCGCTGCTGTGCTCTCGCGCTCAA	410
Query	491	CGCCAGGGTAGCCGACTCAGCTGCGAGGAGATGGGCTTCTCAGGGCACTGACCCACTC	550
Sbjct	411	CGCCAGGGTAGCCGCGCTGAGCTGCGAGGAGATGGGCTTCTCAGGGCTGGCACTC	470
Query	551	CGAGCTGGACGTGCGAACGGCGGGCGCAATGGCACGTCGGGCTTCTCTGTGTTGGACGA	610
Sbjct	471	GGAGCTGGACGTGCGAACGGCGGGCGCAACGGCACGTGGCTTCTCTGCGTGGACGA	530
Query	611	GGGGAGGCTGCCACACCCAGAGGCTGCTGGAGGTACATCTCCGTGTGATTGGCCAG	670
Sbjct	531	GGGGAGGCTGCCGCTGGCCGGAGGTGCTCGAGGTACATCTCCGTGTGACTGTCCCAG	590
Query	671	AGGCCGTTCTGGCCCATCTGCCAAGACTGTGGCCGCAGGAAGCTGCCGTGGACCG	730
Sbjct	591	GGGCCGTTCTGGCTACCGTCTGCCAAGATTGTGGCGAAGGAAGCTGCCGTGGATCG	650
Query	731	CATCGTGGAGGCCAACACAGCTGGCCGGTGGCGAAGTCAGCCTTCGCTA	790
Sbjct	651	CATCGTGGAGGCCAACACAGCTGGCCGGTGGCGAAGTCAGCCTTCGCTA	710
Query	791	TGATGGAGCACACCTCTGTGG-GGGATCCCTGCTCTCGGGGACTGGGTGCTGACAGCCG	849
Sbjct	711	CGATGGAGCACACCTCTGTGGAGGG-TCCCTGCTGTCAGGAGACTGGGTGCTGACAGCCG	769
Query	850	CCCACTGCTTCCGGAGCGGAACCGGGTCTGTCCCAGTGGCGAGTGGTGTGCGGCCG	909

Sbjct	770	CCCACTGCTCCCCGAGCGGAACGGGTCTCTGTCCTGGCGAGTGTGTTGCCGGCGCCG	829
Query	910	TGGCCCGAGGCCCTCTCCCCACGGCTCGCAGCTGGGGTGCAAGGCTGTGGTCTACCAACGGGG	969
Sbjct	830	TGGCCCGAGGCCCTCACCCCATGGCTGCAGCTGGGGTGCAAGGCTGTGGTCTACCAACGGGG	889
Query	970	GCTATCTTCCCTTCGGGACCCCACAGCGAGGAGAACAGCAACGATAATTGCCCTGGTCC	1029
Sbjct	890	GCTACCTCCCTTCGAGACCCCACAGTGAGGAAAACAGCAATGACATTGCCCTGGTCC	949
Query	1030	ACCTCTCCAGTCCCTGCCCCACAGAATACATCCAGCTGTGTCCTCCAGCTGCCG	1089
Sbjct	950	ACCTGTCCAGCCCCCTGCCCTCACAGAGTACATCCAGCCGTGTGTCCTCCGGCGCCG	1009
Query	1090	GCCAGGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGCTGGGCAACACGCACT	1149
Sbjct	1010	GCCAGGGCCCTGGTGGACGGCAAGATCTGCACGGTGACGGCTGGGCAACACGCACT	1069
Query	1150	ATGGCCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATG-TC	1208
Sbjct	1070	ACGGCCAACAGGCTGGGTGCTCCAGGAGGCCGAGTCCCATCATCAGCAACGA-GCTG	1128
Query	1209	TGCAATGGCCTGACTCTATG-GAAACCAGATCAAGCCAAGATGTTCTGTGCTGGCTA	1267
Sbjct	1129	TGCAACGCCCGACTCTACCGCAA-CCAGATCAAGCCAAGATGTTCTGTGCCGGCTA	1187
Query	1268	CCCCGAGGGTGGCATTGATGCCAGGGGACAGCGGTGGTCCCTTGTGAGGAA	1327
Sbjct	1188	CCCCGAGGGCGGCATCGATGCCAGGGGACAGCGGCCCTCTGTGAGGAA	1247
Query	1328	CAGCATCTCGGACGCCACGTTGGCGCTGTGTGGCATTGTGAGTTGGGCACTGGCTG	1387
Sbjct	1248	CAGCATCTCGGACGCCACGTTGGCGCTGTGTGGCATTGTGAGCTGGGCACTGGCTG	1307
Query	1388	TGCCCTGGCCAGAACGCCAGGTCTACACAAAGTCAGTGACTTCCGGAGTGGATCTT	1447
Sbjct	1308	TGCCCTGGCCAGAACGCCAGGTCTACACAAAGTCAGTGACTTCCGGAGTGGATCTT	1367
Query	1448	CCAGGCCATAAAGACTCACTCGAACGCCAGGGCATGGTGACCCAGCTTGACCGGTGGC	1507
Sbjct	1368	CCAGGCCATAAAGACTCACTCGAACGCCAGGGCATGGTGACCCAGCTTGACCGGTGGC	1427
Query	1508	TTCTC---GCTGCGCA-GCCTCCAGGGCCC	1533
Sbjct	1428	TTGTCCTTGATGCGCACGCCCTCAGGGCCC	1457

>ref|XM_001157575.1| PREDICTED: Pan troglodytes hepsin (transmembrane protease, serine 1), transcript variant 2 (HPN), mRNA
Length=1695

GENE ID: 455944 HPN | hepsin (transmembrane protease, serine 1)
[Pan troglodytes]

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 1868 bits (1011), Expect = 0.0	
Identities = 1015/1017 (99%), Gaps = 0/1017 (0%)	
Strand=Plus/Plus	
Query 191 GGTCCCCACCTGGCCCAGGAGGTCAAGCCAGGGAAATCATTAACAAGAGGCAGTGACATGGC	250
Sbjct 146 GGTCCCCACCTGGCCCAGGAGGTCAAGCCAGGGAAATCATTAACAAGAGGCAGTGACATGGC	205
Query 251 GCAGAAAGGAGGGTGGCCGACTGTGCCATGCTGCTCCAGACCCAAGGTGGCAGCTCTCAC	310
Sbjct 206 GCAGAAAGGAGGGTGGCCGACTGTGCCATGCTGCTCCAGACCCAAGGTGGCAGCTCTCAC	265
Query 311 TGCGGGGACCCCTGCTACTTCTGACAGCCATCGGGGCGGCATCTGGGCATTGTGGCTGT	370
Sbjct 266 TGCGGGGACCCCTGCTACTTCTGACAGCCATCGGGGCGGCATCTGGGCATTGTGGCTGT	325
Query 371 TCTCCTCAGGAGTGACCAAGGAGCCGCTGTACCCAGTGCAGGTCAAGCTCTGCCAGCTCG	430
Sbjct 326 TCTCCTCAGGAGTGACCAAGGAGCCGCTGTACCCAGTGCAGGTCAAGCTCTGCCAGCTCG	385
Query 431 GCTCATGGCTTTGACAAGACGGAAGGGACGTGGCGCTGCTGTGCTCTCGCGCTCCAA	490
Sbjct 386 GCTCATGGCTTTGACAAGACGGAAGGGACGTGGCGCTGCTGTGCTCTCGCGCTCCAA	445
Query 491 CGCCAGGGTAGCCGACTCAGCTGCGAGGAGATGGGCTTCTCAGGGCACTGACCCACTC	550
Sbjct 446 CGCCAGGGTAGCCGACTCAGCTGCGAGGAGATGGGCTTCTCAGGGCACTGACCCACTC	505
Query 551 CGAGCTGGACGTGCGAACGGCGGGCGCAATGGCACGTGGCTTCTGTGTGGACGA	610
Sbjct 506 CGAGCTGGACGTGCGAACGGCGGGCGCAATGGCACGTGGCTTCTGTGTGGACGA	565
Query 611 GGGGAGGCTGCCACACCCAGAGGCTGCTGGAGGTCACTCCGTGTGATTGCCAG	670
Sbjct 566 GGGGAGGCTGCCACACCCAGAGGCTGCTGGAGGTCACTCCGTGTGATTGCCAG	625
Query 671 AGGCCGTTCTGGCGCATCTGCCAAGACTGTGGCCAGGAAGCTGCCGTGGACCG	730

Sbjct	626	AGGCCGTTCTTGGCCGCATCTGCCAAGACTGTGGCGCAGGAAGCTGCCCGTGGACCG	685
Query	731	CATCGTGGGAGGCCGGACACCAGCTTGGCGGTGGCGTGGCAAGTCAGCCTTCGCTA	790
Sbjct	686	CATCGTGGGAGGCCGGACACCAGCTTGGCGGTGGCGTGGCAAGTCAGCCTTCGCTA	745
Query	791	TGATGGAGCACACCTCTGTGGGGATCCCTGCTCTCCGGGACTGGGTGCTGACAGCCGC	850
Sbjct	746	TGATGGAGCACACCTCTGTGGGGATCCCTGCTCTCCGGGACTGGGTGCTGACAGCCGC	805
Query	851	CCACTGCTTCCCGAGCGAACCGGGTCTGTCCCAGTGGCAGTGTTGCCGGTCCGT	910
Sbjct	806	CCACTGCTTCCCGAGCGAACCGGGTCTGTCCCAGTGGCAGTGTTGCCGGTCCGT	865
Query	911	GGCCCAGGCCTCTCCCACCGTCTGCAGCTGGGGTGCAGCTGGCTGTGGCTACACAGGGG	970
Sbjct	866	GGCCCAGGCCTCTCCCACCGTCTGCAGCTGGGGTGCAGCTGGCTGTGGCTACACAGGGG	925
Query	971	CTATCTCCCTTTCGGGACCCAAACAGCGAGGAGAACAGCAACGATAATTGCCCTGGTCCA	1030
Sbjct	926	CTATCTCCCTTTCGGGACCCAAACAGCGAGGAGAACAGCAACGATAATTGCCCTGGTCCA	985
Query	1031	CCTCTCAGTCCCCCTGCCCTCACAGAATAACATCCAGCCTGTGTGCCCTCCAGCTGCCG	1090
Sbjct	986	CCTCTCAGTCCCCCTGCCCTCACAGAATAACATCCAGCCTGTGTGCCCTCCAGCTGCCG	1045
Query	1091	CCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGCTGGGAAACACGCACTA	1150
Sbjct	1046	CCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGCTGGGAAACACGCACTA	1105
Query	1151	TGGCCAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGT	1207
Sbjct	1106	TGGCCAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGT	1162

Score = 968 bits (524), Expect = 0.0
 Identities = 528/530 (99%), Gaps = 0/530 (0%)
 Strand=Plus/Plus

Query	1254	TTCTGTGCTGGCTACCCGAGGGTGGCATTGATGCCAGGGCAGCGGGTGGTCCC	1313
Sbjct	1164	TTCTGTGCTGGCTACCCGAGGGTGGCATTGATGCCAGGGCAGCGGGTGGTCCC	1223
Query	1314	TTTGTGTGAGGACAGCATCTCGGACGCCACGTGGCGCTGTGTGGCATTGTGAGT	1373
Sbjct	1224	TTTGTGTGAGGACAGCATCTCGGACGCCACGTGGCGCTGTGTGGCATTGTGAGT	1283
Query	1374	TGGGGCACTGGCTGTGCCCTGGCCAGAACGCCAGGCGTACACCAAAGTCAGTGACTTC	1433
Sbjct	1284	TGGGGCACTGGCTGTGCCCTGGCCAGAACGCCAGGCGTACACCAAAGTCAGTGACTTC	1343
Query	1434	CGGGAGTGGATCTCAGGCCATAAAGACTCACTCGAACGCCAGGGCATGGTACCCAG	1493
Sbjct	1344	CGGGAGTGGATCTCAGGCCATAAAGACTCACTCGAACGCCAGGGCATGGTACCCAG	1403
Query	1494	CTCTGACCGTGGCTTCCTCGCTCGCAGCCTCCAGGGCCGAGGTGATCCGGTGGTGG	1553
Sbjct	1404	CTCTGACCGTGGCTTCCTCGCTCGCAGCCTCCAGGGCCGAGGTGATCCGGTGGTGG	1463
Query	1554	ATCCACGCTGGCCAGGATGGGACGTTTCTTCTTCTGGGCCGGTCCACAGGTCCAAGG	1613
Sbjct	1464	ATCCACGCTGGCCAGGATGGGACGTTTCTTCTTCTGGGCCGGTCCACAGGTCCAAGG	1523
Query	1614	ACACCCCTCCCTCAGGGTCCCTCTTCCACAGTGGCGGGCCACTCAGCCCCGAGACCAC	1673
Sbjct	1524	ACACCCCTCCCTCAGGGTCCCTCTTCCACAGTGGCGGGCCACTCAGCCCCGAGACCAC	1583
Query	1674	CCAACCTCACCCCTCTGACCCCCATGTAATAATTGTTCTGCTGTCTGGACTCCTGTCTA	1733
Sbjct	1584	CCAACCTCACCCCTCTGACCCCCATGTAATAATTGTTCTGCTGTCTGGACTCCTGTCTA	1643
Query	1734	GGTGCCTCTGATGATGGGATGCTTTAAATAAAAGATGGTTTGATT	1783
Sbjct	1644	GGTGCCTCTGATGACGGGATGCTTTAAATAAAAGATGGTTTGATT	1693

>emb|CR597177.1| full-length cDNA clone CS0DJ003YL08 of T cells (Jurkat cell line)
 Cot 10-normalized of Homo sapiens (human)
 Length=1828

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]
 (Over 10 PubMed links)

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position

Score = 1714 bits (928), Expect = 0.0 Identities = 928/928 (100%), Gaps = 0/928 (0%) Strand=Plus/Plus			
Query	533	CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCCAAATGGCACGTGGG	592
Sbjct	375	CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCCAAATGGCACGTGGG	434
Query	593	CTTCTCTGTGTGGACGAGGGAGGCTGCCACACCCAGAGGCTGTGGAGGTATCTC	652

Sbjct	435	CTTCTTCTGTGTGGACGAGGGGAGGCTGCCACACCCAGAGGCTGCTGGAGGTATCTC	494
Query	653	CGTGTGTGATTGCCAGAGGCCCTTCTGGCCGCATCTGCCAAGACTGTGGCCGAG	712
Sbjct	495	CGTGTGTGATTGCCAGAGGCCCTTCTGGCCGCATCTGCCAAGACTGTGGCCGAG	554
Query	713	GAAGCTGCCGTGGACCGCATCGTGGGAGGCCGGACACCAAGCTTGGCCGGTGGCGTG	772
Sbjct	555	GAAGCTGCCGTGGACCGCATCGTGGGAGGCCGGACACCAAGCTTGGCCGGTGGCGTG	614
Query	773	GCAAGTCAGCCTTCGCTATGATGGACACACCTCTGTGGGGATCCCTGCTCTCCGGGA	832
Sbjct	615	GCAAGTCAGCCTTCGCTATGATGGACACACCTCTGTGGGGATCCCTGCTCTCCGGGA	674
Query	833	CTGGGTGCTGACAGCCGCCACTGCTCCCGAGCGAACCGGGTCTGTCCCAGATGGCG	892
Sbjct	675	CTGGGTGCTGACAGCCGCCACTGCTCCCGAGCGAACCGGGTCTGTCCCAGATGGCG	734
Query	893	AGTGTGTTGCCGGTGGCTGGCCCAGGCCCTCCCCACGGTCTGCAGCTGGGGTGCAGGC	952
Sbjct	735	AGTGTGTTGCCGGTGGCTGGCCCAGGCCCTCCCCACGGTCTGCAGCTGGGGTGCAGGC	794
Query	953	TGTGGTCTACCACGGGGCTATCTCCCTTCCGGACCCAAACAGCGAGGAGAACAGCAA	1012
Sbjct	795	TGTGGTCTACCACGGGGCTATCTCCCTTCCGGACCCAAACAGCGAGGAGAACAGCAA	854
Query	1013	CGATATTGCCCTGGTCCACCTCTCCAGTCCCCCTGCCCTCACAGAAATACTCCAGCTGT	1072
Sbjct	855	CGATATTGCCCTGGTCCACCTCTCCAGTCCCCCTGCCCTCACAGAAATACTCCAGCTGT	914
Query	1073	GTGCCTCCAGCTGCCGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGCTG	1132
Sbjct	915	GTGCCTCCAGCTGCCGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGCTG	974
Query	1133	GGGCAAACCGCAGTACTATGGCCAACAGGCCGGGTAECTCCAGGAGGCTCGAGTCCCCAT	1192
Sbjct	975	GGGCAAACCGCAGTACTATGGCCAACAGGCCGGGTAECTCCAGGAGGCTCGAGTCCCCAT	1034
Query	1193	AATCAGCAATGATGCTGCAATGGCGCTGACTTCTATGGAAACCAAGATCAAGCCAAAGAT	1252
Sbjct	1035	AATCAGCAATGATGCTGCAATGGCGCTGACTTCTATGGAAACCAAGATCAAGCCAAAGAT	1094
Query	1253	GTTCTGTGCTGGCTACCCCGAGGGTGGCATTGATGCCAGGGCGACAGCGGTGGTCC	1312
Sbjct	1095	GTTCTGTGCTGGCTACCCCGAGGGTGGCATTGATGCCAGGGCGACAGCGGTGGTCC	1154
Query	1313	CTTTGTGTGAGGACAGCATCTCTGGACAGCCACGTTGGCGCTGTGGCATTGTGAG	1372
Sbjct	1155	CTTTGTGTGAGGACAGCATCTCTGGACAGCCACGTTGGCGCTGTGGCATTGTGAG	1214
Query	1373	TTGGGGCACTGGCTGTGCCCTGGCCAGAACGCCAGGGCTCTACACCAAAGTCAGTGACTT	1432
Sbjct	1215	TTGGGGCACTGGCTGTGCCCTGGCCAGAACGCCAGGGCTCTACACCAAAGTCAGTGACTT	1274
Query	1433	CCGGGAGTGGATCTTCCAGGCCATAAAG	1460
Sbjct	1275	CCGGGAGTGGATCTTCCAGGCCATAAAG	1302

Score = 566 bits (306), Expect = 1e-157
 Identities = 310/312 (99%), Gaps = 0/312 (0%)
 Strand=Plus/Plus

Query	1459	AGACTCACTCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCG	1518
Sbjct	1517	AGACTCACTCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCG	1576
Query	1519	CAGCCTCCAGGGCCCGAGGTGATCCCGGTGGTGGATCCACGCTGGCGAGGATGGGAC	1578
Sbjct	1577	CAGCCTCCAGGGCCCGAGGTGATCCCGGTGGTGGATCCACGCTGGCCTAGGATGGGAC	1636
Query	1579	GTTTTCTTCTGGCCCGGTCCACAGGTCAAAGGACACCCCTCCAGGGTCTCTCT	1638
Sbjct	1637	GTTTTCTTCTGGCCCGGTCCACAGGTCAAAGGACACCCCTCCAGGGTCTCTCT	1696
Query	1639	TCCACAGTGGCGGGCCCACTCAGCCCCGAGACCAACCTCACCTCCTGACCCCCAT	1698
Sbjct	1697	TCCACAGTGGCGGGCCCACTCAGCCCCGAGACCAACCTCACCTCCTGACCCCCAT	1756
Query	1699	GTAAATATTGTTCTGCTGTCTGGACTCCTGCTAGGTGCCCTGATGATGGATGCTCT	1758
Sbjct	1757	GTAAATATTGTTCTGCTGTCTGGACTCCTGCTAGGTGCCCTGATGACGGATGCTCT	1816
Query	1759	TTAAATAATAAA	1770
Sbjct	1817	TTAAATAATAAA	1828

Score = 326 bits (176), Expect = 3e-85
 Identities = 176/176 (100%), Gaps = 0/176 (0%)
 Strand=Plus/Plus

Query	86	CCAGGCCGCCGCTGCTGCCAGGCCACCATGCTCCTGCCAGGCCTGGAGACTGACCCGA	145
Sbjct	1	CCAGGCCGCCGCTGCTGCCAGGCCACCATGCTCCTGCCAGGCCTGGAGACTGACCCGA	60
Query	146	CCCCGGCACTACCTCGAGGCTCCGCCACCTGCTGGACCCAGGGCTCCACCCCTGCC	205

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Sbjct  61    CCCCCGGCACTACCTCGAGGCTCCGCCACCTGCTGGACCCCAGGGTCCCACCCCTGGCC  120
Query  206    CAGGAGGTCAGCCAGGGAAATCATTAAACAAGAGGCAGTGACATGGCGCAGAAGGGAGG  261
Sbjct  121    CAGGAGGTCAGCCAGGGAAATCATTAAACAAGAGGCAGTGACATGGCGCAGAAGGGAGG  176

Score = 244 bits (132), Expect = 8e-61
Identities = 132/132 (100%), Gaps = 0/132 (0%)
Strand=Plus/Plus

Query  405    GTGCAGGTCACTCTCGGGACGCTCGGCTCATGGCTTTGACAAGACGGAAGGGACGTGG  464
Sbjct  176    GTGCAGGTCACTCTCGGGACGCTCGGCTCATGGCTTTGACAAGACGGAAGGGACGTGG  235
Query  465    CGGCTGCTGTGCTCCTCGCGCTCCAACGCCAGGGTAGCCGACTCAGCTGCGAGGAGATG  524
Sbjct  236    CGGCTGCTGTGCTCCTCGCGCTCCAACGCCAGGGTAGCCGACTCAGCTGCGAGGAGATG  295
Query  525    GGCTTCCTCAGG  536
Sbjct  296    GGCTTCCTCAGG  307

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>emb|CR592189.1|  full-length cDNA clone CS0DM012YO15 of Fetal liver of Homo sapiens
(human)
Length=1212

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]
(Over 10 PubMed links)

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

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Score = 1663 bits (900), Expect = 0.0
Identities = 911/916 (99%), Gaps = 2/916 (0%)
Strand=Plus/Plus

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Sbjct  298    GCTTCCTCAAGCGAACCGGGTCCTGTCCCGATGGCGAGTGTGTTGCCGGTGCCGTGGCC  356
Query  915    CAGGCCTCTCCCCACGGTCTGCAGCTGGGGTGCAGGCTGTGGCTACCACGGGGCTAT  974
Sbjct  357    CAGGCCTCTCCCCACGGTCTGCAGCTGGGGTGCAGGCTGTGGCTACCACGGGGCTAT  416
Query  975    CTTCCCTTTCGGGACCCAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCACCTC  1034
Sbjct  417    CTTCCCTTTCGGGACCCAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCACCTC  476
Query  1035   TCCAGTCCCCCTGCCCTCACAGAAATACATCCAGCCTGTGTCCTCCAGCTGCCGCCAG  1094
Sbjct  477    TCCAGTCCCCCTGCCCTCACAGAAATACATCCAGCCTGTGTCCTCCAGCTGCCGCCAG  536
Query  1095   GCCCTGGTGGATGGCAAGATCTGTACCGTGAAGGGCTGGGGCAACACGCAAGTACTATGGC  1154
Sbjct  537    GCCCTGGTGGATGGCAAGATCTGTACCGTGAAGGGCTGGGGCAACACGCAAGTACTATGGC  596
Query  1155   CAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAAT  1214
Sbjct  597    CAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAAT  656
Query  1215   GGCGCTGACTTCTATGGAAACCAAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCCGAG  1274
Sbjct  657    GGCGCTGACTTCTATGGAAACCAAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCCGAG  716
Query  1275   GGTGGCATTGATGCCCTGCCAGGGCGACAGCGGTGGTCCCTTGTGTGAGGGACAGCATC  1334
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Query  1335   TCTCGGACGCCACGTTGGCGGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGCCCTG  1394
Sbjct  777    TCTCGGACGCCACGTTGGCGGTGTGGCATTGTGAGTTGGGGCACTGGCTGTGCCCTG  836
Query  1395   GCCCAGAACGCCAGCGTACACCAAAGTCAGTGACTTCCGGAGGGATCTCCAGGCC  1454
Sbjct  837    GCCCAGAACGCCAGCGTACACCAAAGTCAGTGACTTCCGGAGGGATCTCCAGGCC  896
Query  1455   ATAAAGACTCACTCGAACGCCAGCGGCATGGTGACCCAGCTGTGACCGGTGGCTTC  1514
Sbjct  897    ATAAAGACTCACTCGAACGCCAGCGGCATGGTGACCCAGCTGTGACCGGTGGCTTC  956
Query  1515   TGCGCAGGCCACGGGCCCGAGGTGATCCCGGTGGTGGGATCCACCGCTGGGCCAGGATG  1574
Sbjct  957    TGCGCAGGCCACGGGCCCGAGGTGATCCCGGTGGTGGGATCCACCGCTGGGCCAGGATG  1016
Query  1575   GGACGTTTTCTTCTTGGGCCGGTCCACAGGTCCAAGGACACCCCTCCAGGGTCCT  1634
Sbjct  1017   GGACGTTTTCTTCTTGGGCCGGTCCACAGGTCCAAGGACACCCCTCCAGGGTCCT  1076
Query  1635   CTCTTCCACAGTGGCGGGCCCACAGGCCAGACACCCAAACCTCACCCCTCCTGACCC  1694
Sbjct  1077   CTCTTCCACAGTGGCGGGCCCACAGGCCAGACACCCAAACCTCACCCCTCCTGACCC  1136
Query  1695   CCATGTAATATTGTTCTGCTGTCTGGACTCCTGCTAGGTGCCCTGATGATGGGATG  1754

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Sbjct 1137 CCATGTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCCTGATGACGGGATG 1196
 Query 1755 CTCTTTAAATAATAAAA 1770
 Sbjct 1197 CTCTTTAAATAATAAAA 1212

Score = 327 bits (177), Expect = 8e-86
 Identities = 177/177 (100%), Gaps = 0/177 (0%)
 Strand=Plus/Plus

Query 85 TCCAGGCCGCCGCTGCTGCCGGCCACCATGCTCTGCCAGGCCTGGAGACTGACCCG 144
 Sbjct 1 TCCAGGCCGCCGCTGCTGCCGGCCACCATGCTCTGCCAGGCCTGGAGACTGACCCG 60

Query 145 ACCCCGGCACTACCTCGAGGCTCCGCCCCACCTGCTGGACCCAGGGTCCCACCTGGC 204
 Sbjct 61 ACCCCGGCACTACCTCGAGGCTCCGCCCCACCTGCTGGACCCAGGGTCCCACCTGGC 120

Query 205 CCAGGAGGTCAAGCCAGGAATCATTAACAAGAGGCAGTGACATGGCGAGAAGGAGG 261
 Sbjct 121 CCAGGAGGTCAAGCCAGGAATCATTAACAAGAGGCAGTGACATGGCGAGAAGGAGG 177

Score = 244 bits (132), Expect = 8e-61
 Identities = 132/132 (100%), Gaps = 0/132 (0%)
 Strand=Plus/Plus

Query 405 GTGCAGGGTCAGCTCTGCCGGACGCTCGGCTCATGGTCTTGACAAGACGGAAGGGACGTGG 464
 Sbjct 177 GTGCAGGGTCAGCTCTGCCGGACGCTCGGCTCATGGTCTTGACAAGACGGAAGGGACGTGG 236

Query 465 CGGCTGCTGTGCTCCCTCGCGCTCCAACGCCAGGGTAGCCGACTCAGCTGCGAGGAATG 524
 Sbjct 237 CGGCTGCTGTGCTCCCTCGCGCTCCAACGCCAGGGTAGCCGACTCAGCTGCGAGGAATG 296

Query 525 GGCTTCCTCAGG 536
 Sbjct 297 GGCTTCCTCAGG 308

>emb|CU693029.1| Synthetic construct Homo sapiens gateway clone IMAGE:100019300
 3' read HPN mRNA
 Length=1184

Score = 1653 bits (895), Expect = 0.0
 Identities = 1070/1151 (92%), Gaps = 26/1151 (2%)
 Strand=Plus/Minus

Query 355 GGGC-CATTGTGGCTGTTCTCCTCAGGAGTGAC-CAGGAGCCGCTG-TACCCAGTGCAGG 411
 Sbjct 1148 GGGCACATGGTGGGT-TTTTCTCGGGAG-GGCACAGGAGCC-CTGTTA-CCAGGGGAGG 1093

Query 412 TCAGCTCTCGGGACG-CTC-GGCTCATGGTCTTGACAAGACGGAAGGGACGT-GGGGC 468
 Sbjct 1092 TTAACATTG-GGA-GCCTCGGGTTCA-AGTTTTTGACAACAAACGGAAGGGAC-TGGGGGT 1037

Query 469 TGCTGTGCTCTCGCGCTCCAACGCCAGGGTAGCCGACTCAGCTGCGAGGAATGGGCT 528
 Sbjct 1036 TTTTGT-TTCTTTG-GGTCACACCCAGGGAACCCGGA-TTAGCTGCAAGGA-AT-GGCT 982

Query 529 TCCTCAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGGCCATGGCACGT 588
 Sbjct 981 TGCTCAGGGGA-TGACCCGCTCCGAG-GGGACGTGGGGACGGCGGGGCCATGGCAC-T 925

Query 589 CGGGCTCTCTGTGACAGGGGGAGGCTGCCCCAACACCCAGAGGCTGCTGGAGGTCA 648
 Sbjct 924 TGGGGTTTTCTG-GGGACGAGGGAC-CCCCAGACCCAGAGGGCGCTGGAGGTCA 867

Query 649 TCTCCGTGTGTG-ATTGCCCAAGAGGCCGTTCTGGCCGCCATCTGCCAAGACTGTGGC 707
 Sbjct 866 TCTTCG-GGGGAATGGCCCGAGAGGCCGGTTGTGCGGCCATCTGCCAAGACTGTGGC 808

Query 708 CGCAGGAAGCTGCCGTGGACCGCATCGTGGAGGCCGGACACCAGCTTGGCCGGTGG 767
 Sbjct 807 CGCAGGAAGCTGCCGTGGCCCATCGTGGAGGCCGGACGCCAGCTTGGCCGGTGG 748

Query 768 CCGTGGCAAGTCAGCTTCGCTATGATGGAGCACACCTCTGTGGGGATCCCTGCTCTCC 827
 Sbjct 747 CCGTGGCAAGTCAGCTTCGCTATGATGGGGACACCTCTGTGGGGATCCCTGCTCTCC 688

Query 828 GGGGACTGGGTGCTGACAGCCGCCACTGCTTCCGGAGCGGAACCGGGCCTGTCCCCGA 887
 Sbjct 687 GGGGACTGGGTGCTGACAGCCGCCATTGCTTCCGGAGCGGAACCGGGCCTGTCCCCGA 628

Query 888 TGGCGAGTGTGTTGCCGGTGCCGTGGCCAGGCCTCTCCCCACGGTCTGCACTGGGGTG 947
 Sbjct 627 TGGCGAGTGTGTTGCCGGTGCCGTGGCCAGGCCTCTCCCCACGGTCTGCACTGGGGTG 568

Query 948 CAGGCTGTGGTCTACCACGGGGCTATCTTCCCTTCCGGACCCAAACAGCGAGGAGAAC 1007
 Sbjct 567 CAGGCTGTGGTCTACCACGGGGCTATCTTCCCTTCCGGACCCAAACAGCGAGGAGAAC 508

Query 1008 AGCAACGATATTGCCCTGGTCCACCTCTCCAGTCCCCCTGCCCTCACAGAATACATCCAG 1067
 Sbjct 507 AGCAACGATATTGCCCTGGTCCACCTCTCCAGTCCCCCTGCCCTCACAGAATACATCCAG 448

Query 1068 CCTGTGTGCCCTCCAGCTGCCGGCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACG 1127

Sbjct	447	CCTGTGTGCTCCCAGCTGCCGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACG	388
Query	1128	GGCTGGGCAACACGCAGTACTATGGCCAACAGGCCGGGTACTCCAGGAGGCTCGAGTC	1187
Sbjct	387	GGCTGGGCAACACGCAGTACTATGGCCAACAGGCCGGGTACTCCAGGAGGCTCGAGTC	328
Query	1188	CCCATAATCAGCAATGATGTCTGCAATGGCGCTGACTTCTATGGAAACCAGATCAAGCCC	1247
Sbjct	327	CCCATAATCAGCAATGATGTCTGCAATGGCGCTGACTTCTATGGAAACCAGATCAAGCCC	268
Query	1248	AAGATGTTCTGTGCTGGCTACCCGAGGGTGGATTGATGCCCTGCCAGGGCGACAGCGGT	1307
Sbjct	267	AAGATGTTCTGTGCTGGCTACCCGAGGGTGGATTGATGCCCTGCCAGGGCGACAGCGGT	208
Query	1308	GGTCCCTTTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGCTGTGTGGCATT	1367
Sbjct	207	GGTCCCTTTGTGAGGACAGCATCTCTCGGACGCCACGTTGGCGCTGTGTGGCATT	148
Query	1368	GTGAGTTGGGGCACTGGCTGTGCCCTGCCAGAAGCCAGGCGTCTACACCAAAGTCAGT	1427
Sbjct	147	GTGAGTTGGGGCACTGGCTGTGCCCTGCCAGAAGCCAGGCGTCTACACCAAAGTCAGT	88
Query	1428	GACTTCGGGAGTGGATCTTCAGGCCATAAGACTCACTCCGAAGCCAGCGGCATGGTG	1487
Sbjct	87	GACTTCGGGAGTGGATCTTCAGGCCATAAGACTCACTCCGAAGCCAGCGGCATGGTG	28
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>ref|XM_001157514.1| PREDICTED: Pan troglodytes hepsin (transmembrane protease, serine 1), transcript variant 1 (HPN), mRNA
Length=2104

GENE ID: 455944 HPN | hepsin (transmembrane protease, serine 1)
[Pan troglodytes]

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 1476 bits (799), Expect = 0.0
Identities = 803/805 (99%), Gaps = 0/805 (0%)
Strand=Plus/Plus

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Sbjct	767	CA GTGCAGGT CAGCTCTGCCGACGCTCGGCTCATGGTCTTGACAAAGCGAACGGAGGT	826
Query	463	GGCGGCTGCTGTGCTCCTCGCGTCCAAACGCCAGGGTAGCCGACTCAGCTGCGAGGAGA	522
Sbjct	827	GGCGGCTGCTGTGCTCCTCGCGTCCAAACGCCAGGGTAGCCGACTCAGCTGCGAGGAGA	886
Query	523	TGGGCTTCCTCAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGGGGGGCCAATG	582
Sbjct	887	TGGGCTTCCTCAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGGGGGGCCAATG	946
Query	583	GCACGTGGGCTTCTTCTGTGAGGAGGGAGCTGCCACACCCAGAGGCTGCTGG	642
Sbjct	947	GCACGTGGGCTTCTTCTGTGAGGAGGGAGCTGCCACACCCAGAGGCTGCTGG	1006
Query	643	AGGTCACTCCGTGTGATTGCCAGAGGCCGTTCTTGCCGCCATCTGCCAAGACT	702
Sbjct	1007	AGGTCACTCCGTGTGATTGCCAGAGGCCGTTCTTGCCGCCATCTGCCAAGACT	1066
Query	703	GTGGCCGCAGGAAGCTGCCGTGGACCGCATGTGGAGGCCGGACACCAGCTGGCC	762
Sbjct	1067	GTGGCCGCAGGAAGCTGCCGTGGACCGCATGTGGAGGCCGGACACCAGCTGGCC	1126
Query	763	GGTGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGGATCCCTGC	822
Sbjct	1127	GGTGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGGATCCCTGC	1186
Query	823	TCTCCGGGACTGGGTGCTGACAGCCGCCACTGCTTCCGGAGCGGAACCGGGCTGT	882
Sbjct	1187	TCTCCGGGACTGGGTGCTGACAGCCGCCACTGCTTCCGGAGCGGAACCGGGCTGT	1246
Query	883	CCCGATGGCAGGTGTTGCCGTGCCAGGCCCTCTCCCAAGGTCTGCCAGCTGG	942
Sbjct	1247	CCCGATGGCAGGTGTTGCCGTGCCAGGCCCTCTCCCAAGGTCTGCCAGCTGG	1306
Query	943	GGGTGCAGGTGTTGCCGTACCAACGGGGCTATCTCCCTTCTGGGACCCAACAGCGAGG	1002
Sbjct	1307	GGGTGCAGGTGTTGCCGTACCAACGGGGCTATCTCCCTTCTGGGACCCAACAGCGAGG	1366
Query	1003	AGAACAGCAACGATATTGCCCTGGTCCACCTCTCCAGTCCCCTGCCCTCACAGAAATACA	1062
Sbjct	1367	AGAACAGCAACGATATTGCCCTGGTCCACCTCTCCAGTCCCCTGCCCTCACAGAAATACA	1426
Query	1063	TCCAGCCTGTGCTGCCCTCCAGCTGCCGCCAGGCCCTGGTGGATGCAAGATCTGTACCG	1122
Sbjct	1427	TCCAGCCTGTGCTGCCCTCCAGCTGCCGCCAGGCCCTGGTGGATGCAAGATCTGTACCG	1486
Query	1123	TGACGGCTGGGCAACACGCAGTACTATGCCAACAGGCCGGGTACTCCAGGAGGCTC	1182

Sbjct 1487 TGACGGGCTGGGGCAACACGCAGTACTATGGCAAACAGGCCGGGTACTCCAGGAGGCTC 1546
 Query 1183 GAGTCCCCATAATCAGCAATGATGT 1207
 Sbjct 1547 GAGTCCCCATAATCAGCAATGATGT 1571

Score = 968 bits (524), Expect = 0.0
 Identities = 528/530 (99%), Gaps = 0/530 (0%)
 Strand=Plus/Plus

Query 1254 TTCTGTGCTGGCTACCCCGAGGGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTCCC 1313
 Sbjct 1573 TTCTGTGCTGGCTACCCCGAGGGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTCCC 1632
 Query 1314 TTTGTGTGTGAGGA CAGCATCTCGGACGCCACGTTGGCGGCTGTGTGGCATTGTGAGT 1373
 Sbjct 1633 TTTGTGTGTGAGGA CAGCATCTCGGACGCCACGTTGGCGGCTGTGTGGCATTGTGAGT 1692
 Query 1374 TGGGGCACTGGCTGTGCCCTGGCCAGAAGCCAGGCGTACACCAAAGTCAGTGACTTC 1433
 Sbjct 1693 TGGGGCACTGGCTGTGCCCTGGCCAGAAGCCAGGCGTACACCAAAGTCAGTGACTTC 1752
 Query 1434 CGGGAGTGGATCTTCAGGCCATAAAGACTCACTCGAAGGCCAGGGCATGGTGACCCAG 1493
 Sbjct 1753 CGGGAGTGGATCTTCAGGCCATAAAGACTCACTCGAAGGCCAGGGCATGGTGACCCAG 1812
 Query 1494 CTCTGACCGGTGGCTTCTCGCTGCGCAGCCTCCAGGGCCGAGGTGATCCGGTGGTGGG 1553
 Sbjct 1813 CTCTGACCGGTGGCTTCTCGCTGCGCAGCCTCCAGGGCCGAGGTGATCCGGTGGTGGG 1872
 Query 1554 ATCCACGCTGGGCCAGGGATGGGACGTTTTCTTCTTCTGGGCCGGTCCACAGGTCCAAGG 1613
 Sbjct 1873 ATCCACGCTGGGCCAGGGATGGGACGTTTTCTTCTTCTGGGCCGGTCCACAGGTCCAAGG 1932
 Query 1614 ACACCCCTCCCTCCAGGGTCCCTCTTCCACAGTGGCGGGCCACTCAGCCCCGAGACCAC 1673
 Sbjct 1933 ACACCCCTCCCTCCAGGGTCCCTCTTCCACAGTGGCGGGCCACTCAGCCCCGAGACCAC 1992
 Query 1674 CCAACCTCACCCCTCTGACCCCCATGTAATATTGTTCTGCTGTCTGGACTCCTGTCTA 1733
 Sbjct 1993 CCAACCTCACCCCTCTGACCCCCATGTAATATTGTTCTGCTGTCTGGACTCCTGTCTA 2052
 Query 1734 GGTGCCCTGATGATGGGATGCTCTTAAATAATAAGATGGTTTGATT 1783
 Sbjct 2053 GGTGCCCTGATGACGGGATGCTCTTAAATAATAAGATGGTTTGATT 2102

>emb|cu693028.1| Synthetic construct Homo sapiens gateway clone IMAGE:100019300
 5' read HPN mRNA
 Length=1222

Score = 1465 bits (793), Expect = 0.0
 Identities = 972/1052 (92%), Gaps = 38/1052 (3%)
 Strand=Plus/Plus

Query 245 CATGGCGCAGAAGGGAGGGTGGCCGGACTGTGCCATGCTGCTCCAGACCCAAGGTGGCAGC 304
 Sbjct 16 CATGGCGCAGAAGGGAGGGTGGCCGGACTGTGCCATGCTGCTCCAGACCCAAGGTGGCAGC 75
 Query 305 TCTCACTGCGGGGACCTCTGCTACTTCTGACAGCCATCGGGCGGCATCCTGGGCATTGT 364
 Sbjct 76 TCTCACTGCGGGGACCTCTGCTACTTCTGACAGCCATCGGGCGGCATCCTGGGCATTGT 135
 Query 365 GGCTGTTCTCCTCAGGAGTGACCAAGGAGCCGCTGTACCCAGTGCAGGTCAAGCTCTGCGGA 424
 Sbjct 136 GGCTGTTCTCCTCAGGAGTGACCAAGGAGCCGCTGTACCCAGTGCAGGTCAAGCTCTGCGGA 195
 Query 425 CGCTCGGCTCATGGCTTTGACAAGACGGAAGGGACGTGGCGCTGCTGTCTCTCGCG 484
 Sbjct 196 CGCTCGGCTCATGGCTTTGACAAGACGGAAGGGACGTGGCGCTGCTGTCTCTCGCG 255
 Query 485 CTCCAA CGCCAGGGTAGCCGGACTCAGCTGCGAGGGAGATGGGCTTCCCTCAGGGCACTGAC 544
 Sbjct 256 CTCCAA CGCCAGGGTAGCCGGACTCAGCTGCGAGGGAGATGGGCTTCCCTCAGGGCACTGAC 315
 Query 545 CCACCTCGAGCTGGACGTGCGAACGGCGGGCCAATGGCACGTGGCTTCTCTGTGT 604
 Sbjct 316 CCACCTCGAGCTGGACGTGCGAACGGCGGGCCAATGGCACGTGGCTTCTCTGTGT 375
 Query 605 GGACGAGGGGAGGTGCCCCACACCCAGAGGTGCTGGAGGTCACTCTCGTGTGTGATTG 664
 Sbjct 376 GGACGAGGGGAGGTGCCCCACACCCAGAGGTGCTGGAGGTCACTCTCGTGTGTGATTG 435
 Query 665 CCCCAGAGGCCGTTCTGGCGGCCATCTGCAAAGACTGTGGCGCGAGGAAGCTGCCGT 724
 Sbjct 436 CCCCAGAGGCCGTTCTGGCGGCCATCTGCAAAGACTGTGGCGCGAGGAAGCTGCCGT 495
 Query 725 GGACCGCATCGTGGAGGGCGGGACACCAGCTTGGGGCGGTGGCCGTGGCAAGTCAGCCT 784
 Sbjct 496 GGACCGCATCGTGGAGGGCGGGACACCAGCTTGGGGCGGTGGCCGTGGCAAGTCAGCCT 555
 Query 785 TCGCTATGATGGAGCACACCTCTGTGGGGATCCCTGCTCTCCGGGACTGGGTGCTGAC 844
 Sbjct 556 TCGCTATGATGGAGCACACCTCTGTGGGGATCCCTGCTCTCCGGGACTGGGTGCTGAC 615
 Query 845 AGCCGCCACTGCTTCCGGAGCGGAACCGGGCTCTGTCCCGATGGCGAGTGGTGGCG 904

Sbjct	616	AGCCGCCATTGCTTCCGGAGCGAACCGGGCTCTGTCCCAGTGGCAGTGTTGCCGG	675
Query	905	TGCCGTGGCCC-AGGCCTCTCCCAACGGTCTGC-AGCTGGGGTGCAGGCTGTGGCTAC	962
Sbjct	676	TGCCGTGGCCCCAG-CCTCTCCCCCGTCTGCCA-CTGGGGGGCAGGCTGTGGCTAC	733
Query	963	CACGGGGG-CTATCTTCCCTTT-CGGGACCCAAACAGCGAGGAGAACAGCAACGA-TATT	1019
Sbjct	734	C-CGGGGGGCT-TCTTCCCTTTGG-ACCC-ACCCGCGAGGAGAACAGCAACGAATATT	789
Query	1020	GCC-CTGGTCCACCTCTCCAGT-CCCT-GCCCT-CACAGAATAACATCCAGCCTG-TGT	1074
Sbjct	790	GCCTC-GGTTCACCTTTCAGTTCAGGCCCTAACCCA-AATAAAATCCAGCCTGGTGT	847
Query	1075	GCCT-CCCAGCT-GCCGGCCAGGCCCTGGTGGA-TGGCAAGATCTGT-ACCGTGACGGGC	1130
Sbjct	848	GCCTTCCCC-CTTGGCCGCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	906
Query	1131	T-GGGG-CAACACGAGTACTATG-GCCAACAGGCCG-GGGTACTCCAGGAGGCTCGAG-	1185
Sbjct	907	CCGGGGACA-CACCCAGTACTTGCAC-AACCGGCCGGGGGGGGGGGGGGGGGGGGGG	964
Query	1186	TCCCC-ATAATCAGCAA-TGA-TGTCTGAATGGCGCTGACTTCTATGGAAAC-CAGATC	1241
Sbjct	965	TCTCCTATAATAA-CAAATTAATTCTCCAATGGCGCTAACCTCTTGTAACTCCGATC	1023
Query	1242	A-AGCCCAAGATGTTCTGTGCTGG-CTACCCCC	1271
Sbjct	1024	TGACCCCAACAA-GTTTTTGCTTGTCTACCCCC	1054

>dbj|AK095160.1|  Homo sapiens cDNA FLJ37841 fis, clone BRSSN2012081, highly similar to SERINE PROTEASE HEPSIN (EC 3.4.21.-)
Length=2175

GENE ID: 3249 HPN | hepsin (transmembrane protease, serine 1) [Homo sapiens]
(Over 10 PubMed links)

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 1404 bits (760), Expect = 0.0
Identities = 765/767 (99%), Gaps = 1/767 (0%)
Strand=Plus/Plus
Query 695 CCA-AGACTGTGGCCGAGGAAGCTGCCGTGGACCACATCGTGGAGGCCGGACACCA 753
Sbjct 870 CCACAGACTGTGGCCGAGGAAGCTGCCGTGGACCACATCGTGGAGGCCGGACACCA 929
Query 754 GCTTGGGCCGGTGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGG 813
Sbjct 930 GCTTGGGCCGGTGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGG 989
Query 814 GATCCCTGCTCTCCGGGACTGGGTGCTGACAGCCGCCACTGCTTCCGGAGCGGAACC 873
Sbjct 990 GATCCCTGCTCTCCGGGACTGGGTGCTGACAGCCGCCACTGCTTCCGGAGCGGAACC 1049
Query 874 GGGTCCTGTCCCGATGGCAGGTGTTGCCGTGCCGTGGCCAGGGCTCTCCCCACGGTC 933
Sbjct 1050 GGGTCCTGTCCCGATGGCAGGTGTTGCCGTGCCGTGGCCAGGGCTCTCCCCACGGTC 1109
Query 934 TGCAGCTGGGGGTGCGAGCTGTGCTTACACGGGGCTATCTCCCTTCGGGACCCCA 993
Sbjct 1110 TGCAGCTGGGGGTGCGAGCTGTGCTTACACGGGGCTATCTCCCTTCGGGACCCCA 1169
Query 994 ACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCACCTCTCCAGTCCCTGCCCTCA 1053
Sbjct 1170 ACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCACCTCTCCAGTCCCTGCCCTCA 1229
Query 1054 CAGAATAACATCCAGCCTGTGCTCCAGCTGCCGCCAGGCCCTGGTGGATGGCAAGA 1113
Sbjct 1230 CAGAATAACATCCAGCCTGTGCTCCAGCTGCCGCCAGGCCCTGGTGGATGGCAAGA 1289
Query 1114 TCTGTACCGTGACGGCTGGGACACAGCAGTACTATGGCCAACAGGCCGGGTACTCC 1173
Sbjct 1290 TCTGTACCGTGACGGCTGGGACACAGCAGTACTATGGCCAACAGGCCGGGTACTCC 1349
Query 1174 AGGAGGCTGAGTCCCCATAATCAGCAATGATGCTGCAATGGCGCTGACTTCTATGGAA 1233
Sbjct 1350 AGGAGGCTGAGTCCCCATAATCAGCAATGATGCTGCAATGGCGCTGACTTCTATGGAA 1409
Query 1234 ACCAGATCAAGCCCAAGATGTTCTGTGCTGGTACCCCGAGGGTGGCATGGCTGCC 1293
Sbjct 1410 ACCAGATCAAGCCCAAGATGTTCTGTGCTGGTACCCCGAGGGTGGCATGGCTGCC 1469
Query 1294 AGGGCGACAGCGGTGGTCCCTTGTGAGGACAGCAGTCTCTCGGACGCCACGGTGGC 1353
Sbjct 1470 AGGGCGACAGCGGTGGTCCCTTGTGAGGACAGCAGTCTCTCGGACGCCACGGTGGC 1529
Query 1354 GGCTGTGTGGCATTGTGAGTTGGGGACTGGCTGTGCCCTGGCCAGAACGCCAGCGTCT 1413
Sbjct 1530 GGCTGTGTGGCATTGTGAGTTGGGGACTGGCTGTGCCCTGGCCAGAACGCCAGCGTCT 1589
Query 1414 ACACCAAAAGTCAGTGACTTCCGGAGTGGATCTCCAGGCCATAAAG 1460
Sbjct 1590 ACACCAAAAGTCAGTGACTTCCGGAGTGGATCTCCAGGCCATAAAG 1636

Score = 601 bits (325), Expect = 4e-168
 Identities = 325/325 (100%), Gaps = 0/325 (0%)
 Strand=Plus/Plus

Query	1459	AGACTCACTCCGAAGCCAGCGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCG	1518
Sbjct	1851	AGACTCACTCCGAAGCCAGCGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCG	1910
Query	1519	CAGCCTCCAGGGCCCAGGTGATCCCCGTGGTGGATCCACGCTGGCCGAGGATGGGAC	1578
Sbjct	1911	CAGCCTCCAGGGCCCAGGTGATCCCCGTGGTGGGATCCACGCTGGCCGAGGATGGGAC	1970
Query	1579	GTTTTTCTTCTGGGCCCCGTCCACAGGTCCAAGGACACCCCTCCCTCCAGGGTCCTCT	1638
Sbjct	1971	GTTTTTCTTCTGGGCCCCGTCCACAGGTCCAAGGACACCCCTCCCTCCAGGGTCCTCT	2030
Query	1639	TCCACAGTGGCGGGCCCACTCAGCCCCGAGACCACCCAAACCTCACCTCCTGACCCCCAT	1698
Sbjct	2031	TCCACAGTGGCGGGCCCACTCAGCCCCGAGACCACCCAAACCTCACCTCCTGACCCCCAT	2090
Query	1699	GTAAATATTGTTCTGCTGTCTGGACTCTGTCTAGGTGCCCCGTGATGATGGGATGCTCT	1758
Sbjct	2091	GTAAATATTGTTCTGCTGTCTGGACTCTGTCTAGGTGCCCCGTGATGATGGGATGCTCT	2150
Query	1759	TTAAATAATAAAGATGGTTTGATT	1783
Sbjct	2151	TTAAATAATAAAGATGGTTTGATT	2175

Score = 322 bits (174), Expect = 4e-84
 Identities = 174/174 (100%), Gaps = 0/174 (0%)
 Strand=Plus/Plus

Query	363	GTGGCTGTCTCCTCAGGAGTGACCAAGGAGCCGCTGTACCCAGTGCAAGTCAGCTCTGCG	422
Sbjct	159	GTGGCTGTCTCCTCAGGAGTGACCAAGGAGCCGCTGTACCCAGTGCAAGTCAGCTCTGCG	218
Query	423	GACGCTCGGCTCATGGCTTTGACAAGACGGAAGGGACGTGGCGGCTGCTGTGCTCCCTCG	482
Sbjct	219	GACGCTCGGCTCATGGCTTTGACAAGACGGAAGGGACGTGGCGGCTGCTGTGCTCCCTCG	278
Query	483	CGCTCCAACGCCAGGGTAGCCGACTCAGCTGCGAGGAGATGGGCTCCCTCAGG	536
Sbjct	279	CGCTCCAACGCCAGGGTAGCCGACTCAGCTGCGAGGAGATGGGCTCCCTCAGG	332

Score = 233 bits (126), Expect = 2e-57
 Identities = 129/130 (99%), Gaps = 1/130 (0%)
 Strand=Plus/Plus

Query	533	CAGGGCACTGACCCACTCCGAGCTGGACGTGGAACGGCGGGCGCAAATGGCACGTGGG	592
Sbjct	400	CAGGGCACTGACCCACTCCGAGCTGGACGTGGAACGGCGGGCGCAAATGGCACGTGGG	459
Query	593	CTTCTTCTGTGTGGACGAGGGAGGCTGCCACACCCAGAGGCTGCTGGAGGTATCTC	652
Sbjct	460	CTTCTTCTGTGTGGACGAGGGAGGCTGCCACACCCAGAGGCTGCTGGAGGTATCTC	519
Query	653	CGTGTG-TGA	661
Sbjct	520	CGTGTGGTGA	529

Score = 141 bits (76), Expect = 1e-29
 Identities = 76/76 (100%), Gaps = 0/76 (0%)
 Strand=Plus/Plus

Query	288	AGACCCAAGGTGGCAGCTCTCACTGCGGGGACCCCTGCTACTTCTGACAGCCATCGGGCG	347
Sbjct	1	AGACCCAAGGTGGCAGCTCTCACTGCGGGGACCCCTGCTACTTCTGACAGCCATCGGGCG	60
Query	348	GCATCCTGGGCCATTG	363
Sbjct	61	GCATCCTGGGCCATTG	76

Score = 78.7 bits (42), Expect = 9e-11
 Identities = 42/42 (100%), Gaps = 0/42 (0%)
 Strand=Plus/Plus

Query	658	GTGATTGCCAGAGGCCGTTCTGGCGCCATCTGCCAAG	699
Sbjct	657	GTGATTGCCAGAGGCCGTTCTGGCGCCATCTGCCAAG	698

>ref|XM_001093460.1| PREDICTED: Macaca mulatta hepsin (transmembrane protease, serine 1), transcript variant 1 (HPN), mRNA
 Length=2174

GENE ID: 707242 HPN | hepsin (transmembrane protease, serine 1)
 [Macaca mulatta]

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position

Score = 1360 bits (736), Expect = 0.0
 Identities = 757/767 (98%), Gaps = 1/767 (0%)
 Strand=Plus/Plus

Query	695	CCA-AGACTGTGGCCGCAGGAAGCTGCCCGTGGACCGCATTGTGGGAGGCCGGACACCA	753
Sbjct	867	CCACAGACTGTGGCCGCAGGAAGCTGCCCGTGGACCGCATTGTGGGAGGCCGGACACCA	926
Query	754	GCTTGGGCCGGTGGCCGGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGGGG	813
Sbjct	927	GCTTGGGCCGGTGGCCGGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGGGG	986
Query	814	GATCCCTGCTCTCCGGGACTGGGTGCTGACAGCCGCCACTGCTTCCGGAGCGGAACC	873
Sbjct	987	GGTCCCTGCTCTCCGGGACTGGGTGCTGACAGCTGCCACTGCTTCCGGAGCGGAACC	1046
Query	874	GGGTCCCTGTCCCGATGGCAGGTGTTGCCGGTGCCGTGGCCAGGCCCTCTCCACGGTC	933
Sbjct	1047	GGGTCCCTGTCCCGATGGCAGGTGTTGCCGGTGCCGTGGCCAGGCCCTCTCCACGGTC	1106
Query	934	TGCAGCTGGGGGTGCAGGCTGTGGCTAACACGGGGCTATCTCCCTTCGGGACCCCA	993
Sbjct	1107	TGCAGCTGGGGGTGCAGGCTGTGGCTAACACGGGGCTATCTCCCTTCGGGACCCCA	1166
Query	994	ACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCACCTCTCCAGTCCCCTGCCCTCA	1053
Sbjct	1167	ACAGCGAGGAGAACAGCAATGATATTGCCCTGGTCCACCTCTCCAGTCCCCTGCCCTCA	1226
Query	1054	CAGAATAACATCCAGCCTGTTGCTCCAGCTGCCAGTGGCTGGGATGGCAAGA	1113
Sbjct	1227	CAGAATAACATCCAGCCTGTTGCTCCAGCTGCCAGTGGCTGGGAGGGCTGGGATGGCAAGA	1286
Query	1114	TCTGTACCGTGACGGCTGGGCAACACGCAGTACTATGGCAAACAGGCCGGGTACTCC	1173
Sbjct	1287	TCTGTACCGTGACGGCTGGGCAACACGCAGTACTATGGCAAACAGGCCGGGTACTCC	1346
Query	1174	AGGAGGCTCGAGTCCCATAATCAGCAATGATGTCTGCAATGGCGTGAATTCTATGGAA	1233
Sbjct	1347	AGGAGGCTCGAGTCCCATAATCAGCAATGATGTCTGCAATGGCGTGAATTCTATGGAA	1406
Query	1234	ACCAGATCAAGCCAAAGATGTTCTGTGCTGGTACCCCGAGGGTGGCATTTGATGCCCTGCC	1293
Sbjct	1407	ACCAGATCAAGCCAAAGATGTTCTGTGCTGGTACCCCGAGGGTGGCATTTGATGCCCTGCC	1466
Query	1294	AGGGCGACAGCGGTGGCTCCCTTGTTGAGGACAGCATCTCTCGACGCCACGGTGGC	1353
Sbjct	1467	AGGGTGACAGCGGTGGCTCCCTTGTTGAGGACAGCATCTCTCGACGCCACGGTGGC	1526
Query	1354	GGCTGTGTGGCATTGTGAGTTGGGACTGGCTGTGCCCTGGCCAGAACGCCAGCGTCT	1413
Sbjct	1527	GGCTGTGTGGCATTGTGAGCTGGGACTGGCTGTGCCCTGGCCAGAACGCCAGCGTCT	1586
Query	1414	ACACAAAAGTCAGTGACTIONTCCGGGAGTGGATCTTCAAGCCATAAAG	1460
Sbjct	1587	ACACAAAAGTCAGTGACTIONTCCGGGAGTGGATCTTCAAGCCATAAAG	1633

Score = 551 bits (298), Expect = 4e-153
 Identities = 316/325 (97%), Gaps = 0/325 (0%)
 Strand=Plus/Plus

Query	1459	AGACTCACTCCGAAGCCAGCGGCATGGTGAACCGCAGCTCTGACCGGTGGCTCTCGCTGCG	1518
Sbjct	1848	AGACTCACTCCGAAGCCAGCGGCATGGTGAACCGCAGCTCTGACCGGTGGCTCTCGCTGCG	1907
Query	1519	CAGCCTCCAGGGCCCGAGGTGATCCCGGTGGTGGGATCCACGCTGGCCAGGATGGGAC	1578
Sbjct	1908	CAGCCTCCAGGGCCCGAGGTGATCCCGGTGGTGGGATCCACGCTGGCCAGGATGGGAC	1967
Query	1579	GTTTTCTCTGGCCCGGTCCACAGGTCAAGGAACCCCTCCCTCAGGGTCTCT	1638
Sbjct	1968	ATTTTCTCTGGCCCGGTCCACAGGTCAAGGAACCCCTCCCTCAGGGTCTCT	2027
Query	1639	TCCACAGTGGCGGGCCCACCTAGCCCCGAGACCAACCTCACCTCCTGACCCCCAT	1698
Sbjct	2028	TCCACAGTGGCGGGCCCACCTAGCCCCGAGACCAACCCGACCTCACCTCCTGACCCCCGT	2087
Query	1699	GTAAATATTGTTCTGTGCTGGACTCCCTGTCTAGGTGCCCTGATGATGGGATGCTCT	1758
Sbjct	2088	GTAAATATTGTTCTGTGCTGGACTCCCTGTCTAGGTGCCCTGATGACGGGATGCTCT	2147
Query	1759	TTAAATAATAAAGATGGTTTGATT	1783
Sbjct	2148	TTAAATAATAAAGATGGTTTGATT	2172

Score = 300 bits (162), Expect = 2e-77
 Identities = 170/174 (97%), Gaps = 0/174 (0%)
 Strand=Plus/Plus

Query	363	GTGGCTGTTCTCCTCAGGAGTGACCAAGGAGCCGCTGTACCCAGTGCAAGTCAGCTCTGCG	422
Sbjct	158	GTGGCTGTTCTCCTCAGGAGTGACCAAGGAGCCGCTGTACCCAGTGCAAGTCAGCTCTGCG	217
Query	423	GACGCTCGGCTCATGGTCTTGACAAGACCGGAAGGGAGCTGGCGGCTGCTGTGCTCTCG	482
Sbjct	218	GACGCTCGGCTCATGGTCTTGACAAGACCGGAAGGGAGCTGGCGGCTGCTATGCTCTCA	277

Query 483 CGCTCCAACGCCAGGGTAGCCGGA CTCAGCTGCGAGGAGATGGGTTCCCTCAGG 536
 Sbjct 278 CGCTCCAACACCAGGGTAGCCGGA CTCAGCTGCGAGGAGATGGGTTCCCTCAGG 331

Score = 206 bits (111), Expect = 4e-49
 Identities = 124/130 (95%), Gaps = 1/130 (0%)
 Strand=Plus/Plus

Query 533 CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCCCAATGCCACGTCCGG 592
 Sbjct 399 CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCCCAACGGCACGTCAAGG 458

Query 593 CTTCTTCTGTGTGGACGAGGGGAGGCTGCCACACCCAGAGGCTGCTGGAGGTCACTCTC 652
 Sbjct 459 CTTCTTCTGTGTGGACGAGGGGAGGCTGCCACACCCAGAGGCTGCTGGAGGTCACTCTC 518

Query 653 CGTGTG-TGA 661
 Sbjct 519 CGTGTGGTGA 528

Score = 134 bits (72), Expect = 2e-27
 Identities = 74/75 (98%), Gaps = 0/75 (0%)
 Strand=Plus/Plus

Query 289 GACCCAAGGTGGCAGCTCTCACTGCAGGGACCCCTGCTACTTCTGACAGCCATCGGGCGG 348
 Sbjct 1 GACCCAAGGTGGCAGCTCTCACTGCAGGGACCCCTGCTACTTCTGACAGCCATCGGGCGG 60

Query 349 CATCCTGGGCCATTG 363
 Sbjct 61 CATCCTGGGCCATTG 75

>ref|NM_008281.3| Mus musculus hepsin (Hpn), transcript variant 2, mRNA
 Length=1770

GENE ID: 15451 Hpn | hepsin [Mus musculus] (Over 10 PubMed links)

Score = 1303 bits (705), Expect = 0.0
 Identities = 1343/1644 (81%), Gaps = 71/1644 (4%)
 Strand=Plus/Plus

Query 184 ACCCCAGGGTCCCACCCCTGGCCCAGGAGGTAGCCAGGGATCATTAAACAGAGGCAGTG 243
 Sbjct 148 ACCCCAGGGTCCGCCACAGGCCAACAGGTCAACCTGGGAATCATTAAACAGAGTCCTG 207

Query 244 ACATGGCGAGAAGGAGGGTGGCGGACTG-TGCCATGCTGCTCCAGACCCAAGGTGGCA 302
 Sbjct 208 ACAT-G-GC-GAAGGAGGGTGGCGGACTGCGAG-CATGCTGCTCCAGACCCAAGGTGGCA 263

Query 303 GCTCTCACTGCGGGGACCCCTGCTACTTC-TGACAGGCATCGGGGCGGCATCCTGGGCAT 361
 Sbjct 264 GCTCTCATTGTGGTACCCCTGCTG-TTCCTGACAGGCATTGGGGCGCGTCCTGGGCAT 322

Query 362 TGTGGCTGTTCTCCT-CAGGAGTGACCAAGGAGCCGCTGTACCCAGTCAGGTCAAGCTC- 419
 Sbjct 323 TGTGACCATCTACTGCGAG-AGTGACCAAGGAGCCACTGTACCAAGTCAGCTCAG-TCCA 380

Query 420 GCGGACGCTCGGCTCATGGTCTTGACAAGACGGAAGGGA-CGTGGCGCTGCTGTGCTC 478
 Sbjct 381 GGGGACTCACGGCTTGCGGTGTTGACAAGACGGA-GGGAACGTGGAGGCTACTGTGCTC 439

Query 479 CTCGCGCTCCAACGCCAGGGTAGCCGGA CTCAGCTGCGAGGAGATGGGCTCTCAGGGC 538
 Sbjct 440 CTCACGCTCCAATGCCAGGGTGGCAGGGCTCGGCTGTGAGGAGATGGGCTTCTCAGGGC 499

Query 539 ACTGACCCACTCGAGCTGGACGTGCAA CGGGGGGCCAATGCCACGTGGCTTCTT 598
 Sbjct 500 TCTGGCGCAGCTGGAGCTGGATGTGCGCACTGCAGGGGCCAACGGCACATCGGGCTTCTT 559

Query 599 CTGTGTGGACGAGGGGAGG-CTGCCCCACACCCAGAGGGCTGCTGGAGGTCACTCCGTGT 657
 Sbjct 560 TTGCGTGGACGAGGGC-GGACTGCCTCTGGCTCAGAGGTTGCTGGATGTCACTCTGTAT 618

Query 658 GTGATTGCCAGAGGCCATTCTGGCGCCATCTGCCAAGACTGTGCGCAGGAAGC 717
 Sbjct 619 GTGACTGTCTAGAGGCCATTCTGACTGCCACCTGCCAAGACTGTGCGCAGGAAGC 678

Query 718 TGCCCGTGGACCGCAGTGTGGAGGCCGGACACCAG-CTTGGGCCGTGGCGTGGCAA 776
 Sbjct 679 TGCCGGTGGACCGCATTGTGGGGGCCAGGACAGCAGTCT-GGGAAAGTGGCCGTGGCAG 737

Query 777 GTCAGCCTTCGCTATGATGG-AGCACACCTCTGTGGGGATCCCTGCTCTCGGGACTG 835
 Sbjct 738 GTCAGCCTGCGTTATGATGGGACC-CACCTCTGTGGGGTCCCTGCTGTCTGGGACTG 796

Query 836 GGTGCTGACAGCCGCCACTGCTTCCCGGACGGGAACCGGGTCCCTGCTCCGATGGGAGT 895
 Sbjct 797 GGTGCTGACTGCTGCACATTGCTTCCAGAGCGGAACCGGGTCCCTGCTCGGTGGCGAGT 856

Query 896 GTTTGCCGGTGGCGTAGCCCAGG-CCTCTCCCCACGGTCTGCAGCTGGGGTGCAGGCTG 954
 Sbjct 857 ATTTGCTGGTGCTGTAGCCC-GGACCTCACCCATGCTGCAACTGGGGTTCAAGGCTG 915

Query	955	TGGTCTACACGGGGCTATCTCCCTTCGGGACCCAAC - AGCGAGGAGAACAGCAAC	1013
Sbjct	916	TGATCTATCATGGGGCTACCTCCCTTCAGACCTTA - CTATCGACAAAACAGCAAT	974
Query	1014	GATATTGCCCTGGTCACCTCTCAG - TCCCCGCCCTCACAGAATACTCCAGCTGT	1072
Sbjct	975	GACATTGCCCTGGTCACCTCTAGCTCCC - TGCCCTCACAGAATACTCCAGCCAGT	1033
Query	1073	GTGCCTCCAGCTGCCGGCAGGCCCTGGATGGCAAGATCTGTACCGTGACGGGCTG	1132
Sbjct	1034	GTGTCTCCCTGCTGCCGACAGGCCCTGGATGCCAAGGTCTGTACTGTGACGGGCTG	1093
Query	1133	GGGCAACACGCAGTACTATGGCAACAGGCCGGGTAECTCCAGGAGGCTCGAGTCCCCAT	1192
Sbjct	1094	GGGTAACACACAGTCTATGGCAACAGGCTATGGTGTCTCAAGAGGCCGGGTTCCCAT	1153
Query	1193	AATCAGCAATGATGCTGCAATGGCCTGACTTCTATGGAAACCAGATCAAGCCAAGAT	1252
Sbjct	1154	CATAAGCAACGAAGTTGCAACAGGCCGACTCTACGGGAATCAGATCAAGCCAAGAT	1213
Query	1253	GTTCTGTCTGGCTACCCGAGGGTGGCATTGATGCTCTGCCAGGGCGACAGCGGTGGTCC	1312
Sbjct	1214	GTTCTGTCTGGCTATCTGAGGGTGGCATTGATGCGTGCAGGGCACAGTGGAGGCC	1273
Query	1313	CTTTGTGTGAGGACAGCATCTCTGGACGCCACGTTGGCGCTGTGTGGCATTGTGAG	1372
Sbjct	1274	CTTTGTGTGAAAGACAGCATCTCTGGACATCAAGGTGGCGCTATGTGGCATTGTAAG	1333
Query	1373	TTGGGGCACTGGCTGTGCCCTGGCCAGAAGCCAGGGCTTACACAAAGTCAGTGACTT	1432
Sbjct	1334	CTGGGGTACGGGCTGTGCTTGGCCAGGCCAGGAGTGTACACCAAAGTCAGTGACTT	1393
Query	1433	CCGGGAGTGGATCTCCAGGCCATAAGACTCACTCCGAAGCCAGGGCATGGTGACCA	1492
Sbjct	1394	CCGGGAGTGGATCTCAAGGCCATAAGACTCACTCCGAAGCCAGTGGCATGGTGACTCA	1453
Query	1493	GCTCTGA-CCGG--TGG-CT---T-CTC-G--CTGCGC-AGCCTCCAGGGCCGAG--G-	1537
Sbjct	1454	GCCCTGTATCCCGCCTCATCTCGCTCCGTGCTGCAGTCAGATCCAGAGTCAGAGTTGG	1513
Query	1538	T--GAT--C-CC-G-----GTGGTGGGATCCACGCTGGGCG-AGGATGGGACGTTTT	1584
Sbjct	1514	TCTGGTGGCTCCAGGCCACGTGGTAGGCTCCACACTGGCCTCAC-ATGGAATGGTTTC	1572
Query	1585	CTTCTTGGGCCGGTCCACAGGTCCAAGGACACCCCTCCCTCCAGGGCTCTCTTCCACA	1644
Sbjct	1573	CTGCTCAGATCCAGTCCACGGGTCCAAGGATGC--TGGATCCAAGGACTTCTTCCACA	1630
Query	1645	GTGGCGGGCCCCTCACTCAGCCCC-GAGACCAACCAACCTCACCCCTGTGACCCCCATGTAAA	1703
Sbjct	1631	GTGGCGGGCCCCTCAATCCCAGGG-CCATTGG-CCTCACCCCTCCC-ACCCC-ATGTAAA	1686
Query	1704	TATTGTTCTG-CTGCTGGGACTC-CTGCTTAGGT-GCCCTGTGATGG-GATGCTCTT	1759
Sbjct	1687	TATTACTCTGTCC-TCTGGGGGGCCT-CTAGGGAGCCCCT-TG-TGCAGATGCTCTT	1740
Query	1760	TAAAATAAAAGATGGTTTGATT 1783	
Sbjct	1741	TAAAATAAAAGGTGGTTTGATT 1764	

>ref|NM_017112.1| Rattus norvegicus hepsin (Hpn), mRNA
emb|X70900.1|RNHEPA R. norvegicus mRNA for hepsin
Length=1739

GENE ID: 29135 Hpn | hepsin [Rattus norvegicus] (10 or fewer PubMed links)

Score = 1297 bits (702), Expect = 0.0
Identities = 1341/1643 (81%), Gaps = 69/1643 (4%)
Strand=Plus/Plus

Query	184	ACCCCAAGGGTCCCACCTGGCCAGGAGGTCAGCCAGGGATCATTAAACAAGAGGCAGTG	243
Sbjct	123	ACCCCAAGGGTCCGCCAGGCCAACAGGTCAACCTGGGATCATTAAACAAGAGTCCTG	182
Query	244	ACATGGCCAGAAGGAGGGTGGCGGACTGTGCCATGCTGCCAGGCCAGGTGGCAG	303
Sbjct	183	ACAT-G-GC-GAAGGAGGGTGGCGGACTGCCATGCTGTTCCAGACCCAAGGTGGCAG	239
Query	304	CTCTCACTGGGGGACCTGCTACTTC-TGACAGCCATGGGGCGCATCCTGGCCATT	362
Sbjct	240	CTCTCACTGTGGGGACCTGCTG-TTCTGACAGGCCATTGGGCTGCGTCCTGGCCATT	298
Query	363	GTGGCTGTTCTCCT-CAGGAGTGACCAAGGAGCCGCTGTACCCAGTGCAGGTCAAG-CTCTG	420
Sbjct	299	GTGACCATCTACTAC-GGAGTGACCAAGGAGCCACTGTACCAAGTGCAGCTCAGTCCCAG	357
Query	421	CGGACGCTGGCTCATGGTCTTTGACAAGACGGAAGGGGA-CGTGGGGCTGCTGTGCTCC	479
Sbjct	358	-GGACTCTGACTTTGGTGGACAAGACAGA-GGGAACGTGGAGGCTGCTGTGCTCC	415
Query	480	TCGCGCTCAAACGCCAGGGTAGCCGACTCAGCTGCAGGAGATGGCTCCTCAGGGCA	539
Sbjct	416	TCACGCTCAAACGCCAGGGTAGCCGACTCAGCTGCAGGAGATGGCTTCTCAGGGCT	475
Query	540	CTGACCCACTCCGAGCTGGACGTCGCCAACGGCGGCCATGGCACGTCGGCTTCTTC	599

Sbjct	476	CTGGCGCACTCAGAGCTGGATGTGCGAACCGCGGGCGCCAACGGCACATCGGGCTTCTTC	535
Query	600	TGTGTGGACGAGGGGAGG-CTGCCCCACACCCAGAGGCTGCTGGAGGTATCTCCGTGTG	658
Sbjct	536	TGGCTGGACGAGGGC-GGCTGCCTCTGGCTCAGCGTTGCTGGATGTATCTCTGTATG	594
Query	659	TGATTGCCCAAGAGGCCGTTCTGGCGCCATCTGCCAAGACTGTGGCGCAGGAAGCT	718
Sbjct	595	CGACTGTCTAGAGGCCGATTCTGACTGCCACCTGCCAAGACTGTGGCGCAGGAAGCT	654
Query	719	GCCCCTGGACCCCATCGTGGAGGCCGGACACCAGCTGGCCGGTGCCCCGTGCGAAGT	778
Sbjct	655	GCCGGTGGATCGCATTGGGGGGCCAGGACAGCAGGCTGGAAAGATGGCCATGGCAGGT	714
Query	779	CAGCCTTCGCTATGATGG-AGCACACCTCTGTGGGGATCCCTGCTCTCCGGGACTGGG	837
Sbjct	715	CAGCCTGGTTATGATGGGAC-CACCTCTGTGGGGATCCCTGCTGTCCGGGACTGGG	773
Query	838	TGCTGACAGCCGCCACTGCTTCCGGAGCGGAACCGGGCTGTCCGATGGCGAGTGT	897
Sbjct	774	TACTGACCGCTGCACACTGCTTCCAGAGAGGAACCGGGCTGTCTCGGTGGCGAGTAT	833
Query	898	TTGCCGGTGGCGTGGCCAGG-CCTCTCCCCACGGTC-TGCAGCTGGGGTGCAGGCTGT	955
Sbjct	834	TTGCTGGTGTAGCCC-GGACCTCACCTCATGC-CGTCAGCTGGGGTTCAGGCTGT	891
Query	956	GGTCTACACGGGGCTATCTTCCCTTCGGGACCCCAAC-AGCGAGGAGAACAGAACG	1014
Sbjct	892	GATCTATCATGGGGCTACCTTCCCTTCAGAACCTA-CTATGACGAAAACAGCAATG	950
Query	1015	ATATTGCCCTGGTCCACCTCTCCAG-TCCCTGCCCTCACAGAATACATCCAGGCTGTG	1073
Sbjct	951	ACATTGCCCTGGTCCACCTCTAGCTCCC-TGCCTCTCACAGAATACATCCAGGCGTT	1009
Query	1074	TGCTCTCCAGCTGCCGCCAGGGCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGG	1133
Sbjct	1010	TGTCTCCCTGCTGCCGGACAGGCCCTGGTGGACGGCAAGGTCTGTACAGTGACGGGCTGG	1069
Query	1134	GGCAACACGCAGTAATGGCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCATA	1193
Sbjct	1070	GGTAACACACAGTTCTATGGCCAGCAAGCTGTGGTGTCCAAGGAGGCCGGTCCCAC	1129
Query	1194	ATCAGCAATGATGTCTGCAATGGCGTGACTTCTATGAAACCAAGATCAAGCCAAAGATG	1253
Sbjct	1130	ATAAGCAACGAAGTTGCAACAGCCCGACTTCTACGGGAATCAGATAACCCAAAGATG	1189
Query	1254	TTCTGTGCTGGTACCCCGAGGGTGGCATTGATGCTGCCAGGGCAGCGGGTGGTCC-	1312
Sbjct	1190	TTCTGTGCTGGTATCCTGAGGGTGGTATTGATGCTGCCAGGGTACAGCGGAGG-CCA	1248
Query	1313	CTTTGTGTGTGAGGACAGCATCTCGGA-CGCCACGTTGGCGGCTGTGTGGCATTGTGA	1371
Sbjct	1249	CTTTGTATGTGAGGACAGAACTCT-GGAACATCAAGATGGCGGCTCTGCGGATTGTAA	1307
Query	1372	GTTGGGGCACTGGCTGCCCTGGCCCAGAACGCCAGCGCTACACCAAAGTCAGTACT	1431
Sbjct	1308	GCTGGGGTACGGGCTGTGCTTGGCCGGAAAGCCGGAGTGTACACCAAAGTCATTGACT	1367
Query	1432	TCCGGGAGTGGATCTCCAGGCCATAAAGACTCACTCCGAAGGCCAGCGCATGGTACCC	1491
Sbjct	1368	TCCGGGAGTGGATCTCCAGGCCATAAAGACTCACTCCGAAGCTACCGCATGGTAAC	1427
Query	1492	AGCTCTGACCG-G--TG---GCTT-CTC-GC---TGCACGCTCCAGGGCCCGAG--G-	1537
Sbjct	1428	AGCCCTGACCCCGCTCATGCCCTGCCGCTGCTCCAGCATCCAGAGTCAGAGTTGG	1487
Query	1538	T--GAT--C-CCGGT-G---GTGGGA---TCCACGCTGGGCG-AGGATGGGACGTTTT	1584
Sbjct	1488	TCTGGTGGCTCCAGCCGACGTGGCAGGCTCCACACTGGGCTCAC-ATGGAACGGTTTT	1546
Query	1585	CTTCTTGGGCCGGTCCACAGGTCCAAGGACACCCCTCCCTCCAGGGCTCTCTTCCACA	1644
Sbjct	1547	CTGCTCGGATCCAGTCATAGATCCAAGGGATGC---TGGGCTCAAGGACCTCTTCCACA	1604
Query	1645	GTGGCGGGCCCACTCAGCCCC-GAGACCAACCAACCTCACCTCCTGACCCCCATGTAAA	1703
Sbjct	1605	GTGGCGGGCCCACTCAATCCCAGGG-CCATTGG-CCTCACCCCTCCC-ACCCC-ATGTAAA	1660
Query	1704	TATTGTTCTG-CTGCTGGGA-CTCCTGTCTAGGTGCCCTGATGATG-GGATGCTCTTT	1760
Sbjct	1661	TATTACTCTGTCC-TCTGGGGCTGCTTCGAGGCGCCCT--TG-TGCGGATGCTCTTT	1716
Query	1761	AAATAATAAAGATGGTTTGATT 1783	
Sbjct	1717	AAATAATAAAGGTGGTTTGATT 1739	

>gb|AF030065.1|AF030065 Mus musculus serine protease hepsin mRNA, complete cds
Length=1781

GENE ID: 15451 Hpn | hepsin [Mus musculus] (Over 10 PubMed links)

Score = 1280 bits (693), Expect = 0.0
Identities = 1341/1646 (81%), Gaps = 75/1646 (4%)
Strand=Plus/Plus

Query 184 ACCCCAGGGTCCCACCTGGCCAGGAGGTCAGCCAGGAAATCATTAACAAGAGGCAGTG 243

Sbjct	143	ACCCCAGGGTTCCGCCCAACAGGCTAACCTGGGAATCATTAAACAAGAGTCCCTG	202
Query	244	ACATGGCGAGAAGGGGGTGGCGGACTG-TGCCATGCTGCCAGACCCAGGGTGGCA	302
Sbjct	203	ACAT-G-GC-GAAGGGGGTGGCGGACTGCAG-CATGCTGCCAGACCCAGGGTGGCA	258
Query	303	GCTCTCACTGCGGGGACCCCTGCTACTTC-TGACAGCCATCGGGGCGCATCTGGCCAT	361
Sbjct	259	GCTCTCATGGTGGGTACCCCTGCTG-TTCCTGACAGGCCATTGGGGCGCTCTGGCCAT	317
Query	362	TGTGGCTGTCTCCT-CAGGAGTGACCAGGAGCCGCTGTACCCAGTCAGGTCAGCTCT-	419
Sbjct	318	TGTGACCATCTACTGCAG-AGTGACCAGGAGCCACTGTACCAAGTGCAGCTCAG-TCCA	375
Query	420	GGGGACGCTCGGCT--CATGGTCTTGACAAGACGGAAGGG-ACGTGGCGGCTGCTGTGC	476
Sbjct	376	GGGGACTCACGACTTGCA-G-TGTTGGACAAGACGGA-GGGTACGTGGAGGCTACTGTGC	432
Query	477	TCCTCGCGCTCAAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGATGGCTTCCTCAGG	536
Sbjct	433	TCCTCACGCCATGCCAGGGTGGCAGGGCTCGGCTGTGAGGAGATGGCTTCCTCAGG	492
Query	537	GCACTGACCCACTCGAGCTGGACGTGCGAACGGCGGCCAATGGCACGTCGGCTTC	596
Sbjct	493	GCTCTGGCGCAGCTGGAGCTGGATGTGCGCAGTCGGGCCAACGGCACATCGGGCTTC	552
Query	597	TTCTGTGTGGACGAGGGGAGG-CTGCCCCACACCCAGAGGCTGCTGGAGGTCATCTCCGT	655
Sbjct	553	TTTTCGCTGGACGAGGGC-GGACTGCCTCTGGCTCAGAGGTTGCTGGATGTCATCTGT	611
Query	656	GTGTGATTGCCAGAGGGCGTTCTTGGCCCATCTGCCAACAGACTGTGGCCGAGGAA	715
Sbjct	612	ATGTGACTGTCCTAGAGGCCATTCTGACTGCCACCTGCCAACAGACTGTGGCCGAGGAA	671
Query	716	GCTGCCCTGGACCGCATCGTGGAGGGCCGGACACCAG-CTTGGGCCGTGGCGTGGC	774
Sbjct	672	GCTGCCCTGGACCGCATGTGGGGGGCAGGACAGCAGTCT-GGGAGGTGGCGTGGC	730
Query	775	AAGTCAGCCTCGCTATGATGG-AGCACACCTCTGTTGGGATCCCTGCTCTCGGGGAC	833
Sbjct	731	AAGTCAGCCTCGCTATGATGGGACC-CACCTCTGTTGGGATCCCTGCTCTGGGAC	789
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Sbjct	790	TGGGTGCTGACTGCTGCACATTGCTTTCCAGAGCGGAACCGGGTCTGTCTCGGTGGCGA	849
Query	894	GTGTTTGCCTGGCTGCCAGG-CCTCTCCCCACGGTCTGCACTGGCTGGGGTCCAGGC	952
Sbjct	850	GTATTGCTGGTGTGCTAGCCC-GGACCTCACCCATGCTGTGCAACTGGGGTTCAGGC	908
Query	953	TGTGGTCTACCACGGGGCTATCTCCCTTTCGGGACCCAAAC-AGCGAGGAGAACAGCA	1011
Sbjct	909	TGTGATCTATCATGGGGCTACCTCCCTTTCGAGACCCCA-CTATTGACGAAAACAGCA	967
Query	1012	ACGATAATTGCCCTGGTCCACCTCTCCAG-TCCCTGCCCTCACAGAAATACATCCAGCCT	1070
Sbjct	968	ATGACATTGCCCTGGTCCACCTCTAGCTCCC-TGCCCTCACAGAAATACATCCAGCCA	1026
Query	1071	GTGTGCCCTCCAGCTGCCGGCAGGCCCTGGTGGATGGAAGATCTGTACCGTGACGGGC	1130
Sbjct	1027	GTGTGCTCCCTGCTGCCGGACAGGCCCTGGTGGATGGAAGGTCTGTACTGTGACGGGC	1086
Query	1131	TGGGGCAACACGCAGTACTATGGCAAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCC	1190
Sbjct	1087	TGGGGTAACACACAGTTCTATGCCAACAGGCTATGGTGTCTCAAAGAGGCCGGTTCCC	1146
Query	1191	ATAATCAGCAATGATGTCGCAATGGCGCTGACTTCTATGGAACCAAGATCAAGCCAAAG	1250
Sbjct	1147	ATCATAAGCAACGAAGTTGCAACAGCCCCGACTCTACGGGAATCAGATCAAGCCAAAG	1206
Query	1251	ATGTTCTGTGCTGGCTACCCGGAGGGTGGCATTGATGCCCTGCCAGGGCACAGCGTGGT	1310
Sbjct	1207	ATGTTCTGTGCTGGCTACCTGAGGGTGGCATTGATGCGTGCCAGGGCACAGTGGAGGC	1266
Query	1311	CCCTTGTGTGAGGACAGCATCTCTGGACGCCACGGTGGCGGTGTGTCATTGTG	1370
Sbjct	1267	CCCTTGTGTGAGGACAGCATCTCTGGACATCAAGTGGCGGTATGTGGCATTGTA	1326
Query	1371	AGTTGGGGCACTGGCTGTCCTGGCCAGAGCCAGGCGTCTACACCAAAGTCAGTGAC	1430
Sbjct	1327	AGCTGGGGTACCGGCTGTGCTTGGCCCGGAAGCCAGGAGTGTACACCAAAGTCAGTGAC	1386
Query	1431	TTCCGGGAGTGGATCTTCAGGCCATAAGACTCACTCCGAAGGCCAGCGGATGGTAC	1490
Sbjct	1387	TTCCGGGAGTGGATCTCAAGGCCATAAGACTCACTCCGAAGGCCAGTGGCATGGTAC	1446
Query	1491	CAGCTCTGA-CCGG--TGG-CT---T-CTC-G--CTGCGC-AGCCTCCAGGGCCGAG--	1536
Sbjct	1447	CAGCCCTGATCCCGCTCATCTCGCTGCCAGTCAGTCAACTAGCATCCAGAGTCAGAGTT	1506
Query	1537	G-T--GAT--C-CC-G-----GTGGTGGGATCCACGCCAGGGCG-AGGATGGGACGTT	1582
Sbjct	1507	GGTCTGGTGGCTCCAGCCCCACGTGGTAGGCTCCACACTGGGCTCAC-ATGGAATGGTT	1565
Query	1583	TTCTTCTGGGCCGGTCCACAGGTCCAAGGACACCCCTCCCTCCAGGGTCCTCTTCCA	1642
Sbjct	1566	TCCTGCTCAGATCCAGTCCACGGGTCAGGATGC-TGGATCCAAGGACTCTCTTCCA	1623

Query	1643	CAGTGGCGGGCCCACTCAGCCCC-GAGACCACCCAAACCTCACCCCTCTGACCCCCATGTA	1701
Sbjct	1624	CAGTGGCGGGCCCACTCATCCCAGGG-CCATTGG-CCTCACCCCTCCC-ACCCC-ATGTA	1679
Query	1702	AATATTGTTCTG-CTGTCTGGGACTC-CTGTCTAGGT-GCCCTGTATGATGG-GATGCTC	1757
Sbjct	1680	AATATTACTCTGTCC-TCTGGGGGGCCT-CTAGGGAGCCCT-TG-TGCAGATGCTC	1733
Query	1758	TTTAAATAAAAGATGGTTTGATT	1783
Sbjct	1734	TTTAAATAAAAGTGGTTTGATT	1759

>ref|NM_001110252.1| Mus musculus hepsin (Hpn), transcript variant 1, mRNA
Length=1830

GENE ID: 15451 Hpn | hepsin [Mus musculus] (Over 10 PubMed links)

Score = 1245 bits (674), Expect = 0.0
Identities = 1282/1569 (81%), Gaps = 68/1569 (4%)
Strand=Plus/Plus

Query	259	AGGGTGGCGGACTG-TGCCATGCTGCTCCAGACCAAGGTGGCAGCTCTCACTGCGGGG	317
Sbjct	280	AGGGTGGCGGACTGCAG-CATGCTGCTCCAGACCAAGGTGGCAGCTCTCATTGCGGT	338
Query	318	ACCCCTGCTACTTC-TGACAGCCATCGGGCGGGCATCCTGGGCCATTGTGGCTGTTCTCCT	376
Sbjct	339	ACCCCTGCTG-TTCCTGACAGGCATTGGGGCGCGTCTGGGCCATTGTGACCATCCTACT	397
Query	377	-CAGGAGTGACCAGGAGCCGCTGTACCCAGTGCAGGTCACTCT-GCGGACGCTCGGCTC	434
Sbjct	398	GCAG-AGTGACCAGGAGCCACTGTACCAAGTGCAGCTCAG-TCCAGGGACTCACGGCTT	455
Query	435	ATGGTCTTGAACAAGACGGAAGGGA-CGTGGCGGCTGCTGTGCTCCTCGCGCTCCAACGC	493
Sbjct	456	GCGGTGTTGAACAAGACGGA-GGAAACGTGGAGGCTACTGTGCTCCTCACGCTCCAATGC	514
Query	494	CAGGGTAGCGGACTCAGCTGCGAGGAGATGGGCTTCCCTCAGGGCACTGACCCACTCCGA	553
Sbjct	515	CAGGGTGGCAGGGCTGGCTGTGAGGAGATGGGCTTCTCAGGGCTCTGGCGACTCGGA	574
Query	554	GCTGGACGTGCAAACGGCGGGGCCAATGGCACGTGGCTTCTCTGTGTGGACGAGGG	613
Sbjct	575	GCTGGATGTGCGCACTGGGGGCCAACGGCACATCGGGCTTCTTGTGGACGAGGG	634
Query	614	GAGG-CTGCCCCACACCCAGAGGCTGCTGGAGGTATCTCCGTGTGATTGCCAGAG	672
Sbjct	635	C-GGACTGCTCTGGCTCAGAGGTGCTGGATGTATCTGTATGTGACTGTCTAGAG	693
Query	673	GCCGTTTCTGGCCGCATCTGCAAAGACTGTGGCCGCAGGAAGCTGCCGTGGACCGCA	732
Sbjct	694	GCCGATTCTGACTGCCACCTGCCAACACTGTGGCCGCAGGAAGCTGCCGTGGACCGCA	753
Query	733	TGTTGGGAGGCCGGACACCAG-CTTGGGCCGTGGCGTGGCAAGTCAGCCTTCGCTAT	791
Sbjct	754	TTGTGGGGGCCAGGACAGCAGTCT-GGAAAGGTGGCGTGGCAGGCTAGCCTGGCTTAT	812
Query	792	GATGG-AGCACACCTCTGTGGGGATCCCTGCTCTCAGGGACTGGGTGCTGACAGCCG	850
Sbjct	813	GATGGGACC-CACCTCTGTGGGGGTCCTGCTGTCTGGGACTGGGTGCTGACTGCTGC	871
Query	851	CCACTGCTTCCGGAGCGGAACCGGGTCTGTCCCAGTGGCAGTGTTGCCGTGCCGT	910
Sbjct	872	ACATTGCTTCCAGAGCGGAACCGGGTCTGTCTGGCTGGCAGTATTGCTGGTGT	931
Query	911	GGCCCAAGG-CCTCTCCCCACGGCTGAGCTGGGGTGCAAGGCTGTGGCTACCAACGGG	969
Sbjct	932	AGCCC-GGACCTCACCCATGCTGTGCAAATGGGGTTCAAGGCTGTGATCTATCATGGG	990
Query	970	GCTATCTCCCTTTCGGACCCAAAC-AGCGAGGAGAACAGCAACGATATTGCCCTGGTC	1028
Sbjct	991	GCTACCTTCCCTTCGGAGACCCCTA-CTATCGACGAAAACAGCAATGACATTGCCCTGGTC	1049
Query	1029	CACCTCTCCAG-TCCCTGCCCTCACAGAAATACATCCAGCCTGTGTGCCCTCCAGCTGC	1087
Sbjct	1050	CACCTCTCTAGCTCCC-TGCCTCTCACAGAAATACATCCAGCCTGTGTGCCCTGCTGC	1108
Query	1088	CGGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGCAACACCGAGTA	1147
Sbjct	1109	GGGACAGGCCCTGGTGGATGGCAAGGTCTGTACTGTGACCGGCTGGGTAACACACAGTT	1168
Query	1148	CTATGGCCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCATAATCAGCAATGATGT	1207
Sbjct	1169	CTATGGCCAACAGGCTATGGTGTCCAAAGAGGCCGGGTTCCATATAAGCAACGAAGT	1228
Query	1208	CTGCAATGGCGCTGACTTCTATGAAACCAGATCAAGCCAAAGATGTTCTGTGCTGGCTA	1267
Sbjct	1229	TTGCAACAGGCCCGACTTCTACGGAAATCAGATCAAGCCAAAGATGTTCTGTGCTGGCTA	1288
Query	1268	CCCCGAGGGTGGCATTGATGCGCTGCCAGGGCGACAGCGGTGGTCCCTTGTGTGAGGA	1327
Sbjct	1289	TCCTGAGGGTGGCATTGATGCGTGCAGGGCGACAGTGGAGGCCCTTGTGTGAGGA	1348
Query	1328	CAGCATCTCGGACGCCACGTTGGCGGCTGTGTGGCATTGTGAGGTGGGGCACTGGCTG	1387

Sbjct	1349	CAGCATCTCTGGGACATCAAGGTGGCGGCTATGTGGCATTGTAAGCTGGGTACGGGCTG	1408
Query	1388	TGCCCTGGCCAGAACGCCAGCGCTCACACCAAAGTCAGTGACTTCCGGAGTGGATCTT	1447
Sbjct	1409	TGCTTTGGCCCGGAAGCCAGGAGTGTACACCAAAGTCAGTGACTTCCGGAGTGGATCTT	1468
Query	1448	CCAGGCCATAAAGACTCACTCGAAGGCAGCGGCATGGTACCCAGCTCTGA-CCGG--T	1504
Sbjct	1469	CAAGGCCATAAAGACTCACTCGAAGGCAGTGCACTGGTACCTAGCCCTGATCCGCCT	1528
Query	1505	GG-CT---T-CTC-G--CTGCGC-AGCCTCAGGGCCCAG--G-T-GAT-C-CC-G-	1545
Sbjct	1529	CATCTCGTGTCCGTGCTGCACTAGCATCCAGAGTCAGAGTTGGTCTGGTGGCTCCAGC	1588
Query	1546	-----GTGGTGGGATCCACGCTGGGCCAGGATGGGACGTTTTCTCTTCTGGGGCCGGT	1599
Sbjct	1589	CCCACGTGGTAGGCTCCACACTGGGCTCAC-ATGGAATGGTTCTGCTCAGATCCAGT	1647
Query	1600	CCACAGGTCCAAGGACACCCCTCCCTCAGGGCCTCTCTTCCACAGTGGCGGGCCACTC	1659
Sbjct	1648	CCACGGGTCCAAGGATGC--TGGATCCAAGGACTCTCTTCCACAGTGGCGGGCCACTC	1705
Query	1660	AGCCCC-GAGACCACCAACCTCACCTCTGACCCCATGTAATATTGTTCTG-CTGT	1717
Sbjct	1706	AATCCCAGGG-CCATTGG-CCTCACCCCTCCC-ACCCC-ATGTAATATTACTCTGTCC-T	1760
Query	1718	CTGGGACTC-CTGTCTAGGT-GCCCTGATGATGG-GATGCTCTTAAATAATAAGATG	1774
Sbjct	1761	CTGGGGGGCGCT-CTAGGGAGCCCT--TG-TGCAGATGCTCTTAAATAATAAGGTG	1815
Query	1775	GTTTGATT 1783	
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>gb|BC138809.1| Mus musculus hepsin, mRNA (cDNA clone MGC:170436 IMAGE:8861831), complete cds Length=1505

Score = 1240 bits (671), Expect = 0.0
Identities = 1075/1271 (84%), Gaps = 23/1271 (1%)
Strand=Plus/Plus
Query 259 AGGGTGGCCGGACTG-TGCCATGCTGCTCCAGACCCAAGGTGGCAGCTCTCACTGCGGG 317
Sbjct 160 AGGGTGGCCGGACTGCAG-CATGCTGCTCCAGACCCAAGGTGGCAGCTCTCATTGGGT 218
Query 318 ACCCTGCTACTTC-TGACAGCCATCGGGCGGCATCCTGGGCATTGGCTGTTCTCCT 376
Sbjct 219 ACCCTGCTG-TTCTGACAGGCATTGGGCGCGTCCTGGGCATTGTGACCATCCTACT 277
Query 377 -CAGGAGTGACCAGGAGCCGCTGTACCACTGAGCTCT-GCGGACGCTCGGCTC 434
Sbjct 278 GCAG-AGTGACCAAGGAGCCACTGTACCAAGTGCAGCTCG-A-TCCAGGGACTCACGGCTT 335
Query 435 ATGGTCTTGAACAAGCGGAAGGGA-CGTGGCGCTGCTGTGCTCTCGCCTCCAACGC 493
Sbjct 336 GCGGTGTTGAACAAGCGGA-GGGAACGTGGAGGCTACTGTGCTCTCACGCTCCAATGC 394
Query 494 CAGGGTAGCCGGAACAGCTGCGAGGAGATGGCTTCTCAGGGCACTGACCCACTCCGA 553
Sbjct 395 CAGGGTGGAGGGCTGGCTGTGAGGAGATGGCTTCTCAGGGCTCTGGCGCACTCGGA 454
Query 554 GCTGGACGTGCGAACGGCGGCCATGGCACGTGGCTTCTCTCTGTGTGGACGAGGG 613
Sbjct 455 GCTGGATGTGCGCACTGGGGCGCAACGGCACATGGCTTCTTTGGCTGGACGAGGG 514
Query 614 GAGG-CTGCCCCACACCCAGAGGCTGCTGGAGGTATCTCGTGTGTGATTGCCCGAGAG 672
Sbjct 515 C-GGACTGCTCTGGCTCAGAGTTGCTGGATGTATCTGTATGTACTGCTTAGAG 573
Query 673 GCCGTTCTGGCGCCATCTGCAAGACTGTGGCCGAGGAAGCTGCCGTGGACCGCA 732
Sbjct 574 GCCGATTCTGACTGCCACCTGCCAAGACTGTGGCCGAGGAAGCTGCCGTGGACCGCA 633
Query 733 TCGTGGGAGGCCGGACACCAAG-CTTGGCCGGTGGCGTGGCAAGTCAGCCTTCGCTAT 791
Sbjct 634 TTGTGGGGGCCAGGAACGGACTCT-GGGAAGGTGGCCGTGGCAGGTAGCCTGGTTAT 692
Query 792 GATGG-AGCACACCTCTGTGGGGATCCCTGCTCTCGGGGACTGGTGCTGACAGCCGC 850
Sbjct 693 GATGGGACC-CACCTCTGTGGGGGTCCCTGCTGTCTGGGACTGGTGCTGACTGCTGC 751
Query 851 CCACTGCTTCCCGAGCGGAACCGGGTCTGTCCCGATGGCAGGTGGTGTGGCTGGCGT 910
Sbjct 752 ACATTGCTTCCAGAGCGGAACCGGGTCTGTCTGGCAGGTGGTGTGGCTGT 811
Query 911 GGCCCAAGG-CCTCTCCCCACGGTCTGCAGCTGGGGTGCAGGCTGTGGCTACACGGGG 969
Sbjct 812 AGCCC-GGACCTCACCCCATGCTGTGCAACTGGGGTTCAAGGCTGTGATCTATCATGGGG 870
Query 970 GCTATCTCCCTTCGGGACCCAAAC-AGCGAGGAGAACAGCAACGATATTGCCCTGGTC 1028
Sbjct 871 GCTACCTTCCCTTCGAGACCCTA-CTATCGACGAAACAGCAATGACATTGCCCTGGTC 929
Query 1029 CACCTCTCCAG-TCCCTGCCCCCTCACAGAATACATCCAGCCTGTGTGCTCCAGCTGC 1087
Sbjct 930 CACCTCTCTAGCTCCC-TGCCTCTCACAGAATACATCCAGCCAGTGTGTCTCCCTGCTGC 988

Query	1088	CGGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGCAACACCGAGTA	1147
Sbjct	989	GGGACAGGCCCTGGTGGATGGCAAGGTCTGTACTGTGACCGGCTGGGTAACACAGTT	1048
Query	1148	CTATGGCCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCATAATCAGCAATGATGT	1207
Sbjct	1049	CTATGGCCAACAGGCTATGGTCTCAAGAGGCCGGTCCCATAAGCAACGAAGT	1108
Query	1208	CTGCAATGGCGCTGACTCTATGAAACCAGATCAAGCCAAGATGTTCTGTGCTGGCTA	1267
Sbjct	1109	TTGCAACAGGCCCGACTCTACGGGAATCAGATCAAGCCAAGATGTTCTGTGCTGGCTA	1168
Query	1268	CCCCGAGGGTGGCATTGATGCCTGCCAGGGCGACAGCGGTGGTCCCTTGTGTGAGGA	1327
Sbjct	1169	TCCTGAGGGTGGCATTGATGCGTGCCAGGGCGACAGTGGAGGCCCTTGTGTGAGGA	1228
Query	1328	CAGCATCTCTCGGACGCCACGTTGGCGCTGTGTGGCATTGTGAGTTGGGGCACTGGCTG	1387
Sbjct	1229	CAGCATCTCTGGGACATCAAGGTGGCGCTATGTGGCATTGTAAGCTGGGTACGGGCTG	1288
Query	1388	TGCCCTGGCCAGAACGCCAGCGTCTACACCAAAGTCAGTGACTTCCGGAGTGGATCTT	1447
Sbjct	1289	TGCTTGGCCCGGAAGCCAGGAGTGTACACCAAAGTCAGTGACTTCCGGAGTGGATCTT	1348
Query	1448	CCAGGCCATAAAGACTCACTCGAACGCCAGCGGCATGGTGAACCCAGCTCTGA-CCGGTGG	1506
Sbjct	1349	CAAGGCCATAAAGACTCACTCGAACGCCAGTGGCATGGTACTCAGCCGTATCCGCCT	1408
Query	1507	CTTCTCGCTGC 1517	
Sbjct	1409	CATCTCGCTGC 1419	

>dbj|AK156553.1| Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830029I12 product:hepsin, full insert sequence
Length=1745

GENE ID: 15451 Hpn | hepsin [Mus musculus] (Over 10 PubMed links)

Score = 1240 bits (671), Expect = 0.0
Identities = 1282/1570 (81%), Gaps = 70/1570 (4%)
Strand=Plus/Plus

Query	259	AGGGTGGCCGGACTG-TGCCATGCTGCTCCAGACCCAAGGTGGCAGCTCTCACTGGGGG	317
Sbjct	195	AGGGTGGCCGGACTGCAG-CATGCTGCTCCAGACCCAAGGTGGCAGCTCTCATTGGGT	253
Query	318	ACCCCTGCTACTTC-TGACAGCCATCGGGCGGCATCCTGGGCATTGTGGCTGTTCTCCT	376
Sbjct	254	ACCCCTGCTG-TTCCCTGACAGGCAATTGGGCGCGTCTGGGCATTGTGACCATCCTACT	312
Query	377	-CAGGAGTGACCAGGAGCCGCTTACCCAGTGCAGG-TCAAGCTCT-GCGGACGCTCGGCT	433
Sbjct	313	GCAG-AGTGACCAGGAGCCACTGTACCAAGTGCA-GGCTCAG-TCCAGGGACTCACGGCT	369
Query	434	CATGGTCTTGACAAGACCGGAAGGGA-CGTGGCGGCTGCTGTGCTCTCGCGCTCCAACG	492
Sbjct	370	TGCGGTGTTGACAAGACCGGA-GGGAACGTGGAGGCTACTGTGCTCTCACGCTCCAATG	428
Query	493	CCAGGGTAGCCGGACTCAGCTGCGAGGAGATGGGCTTCCTCAGGGCACTGACCCACTCCG	552
Sbjct	429	CCAGGGTGGCAGGGCTCGCTGTGAGGGAGATGGGCTTCAGGGCTCTGGCACACTCGG	488
Query	553	AGCTGGACGTGCGAACGGCGGGCGCCAATGGCACGTGGCTTCTCTGTGTGGACGAGG	612
Sbjct	489	AGCTGGATGTGCGACTGCGGCCAACGGCACATCGGGCTTCTTGTGGACGAGG	548
Query	613	GGAGG-CTGCCACACCCAGAGGCTGCTGGAGGTCACTCCGTGTGTGATTGCCAGA	671
Sbjct	549	GC-GGACTCTGCTCTGGCTCAGAGGTTGCTGGATGTCACTCTGTATGTGACTGTCTAGA	607
Query	672	GGCGTTTCTGGCCGCCATCTGCCAACGACTGTGGCGCAGGAAGCTGCCGTGGACCGC	731
Sbjct	608	GGCGGATTCTGACTGCCAACCTGCCAACGACTGTGGCGCAGGAAGCTGCCGTGGACCGC	667
Query	732	ATCGTGGAGGCCGGACACCAAG-CTTGGGCCGGTGGCGTGGCAAGTCAGCCTTCGCTA	790
Sbjct	668	ATTGTGGGGGCCAGGACAGCAGTCT-GGGAAAGGTGGCGTGGCAGGTCAAGCTCGCTTA	726
Query	791	TGATGG-AGCACACCTCTGTGGGGATCCCTGCTCTCGGGGACTGGGTGCTGACAGCCG	849
Sbjct	727	TGATGGGA-CTCACCTCTGTGGGGTCCCTGCTGTCTGGGACTGGGTGCTGACTGCTG	785
Query	850	CCCACTGCTTCCGGAGCGGAACCGGGCTCTGTCCGATGGCGAGTGTGTTGCCGGTGGCG	909
Sbjct	786	CACATTGCTTCCAGCGGAACCGGGTCCCTGCTCGGTGGCGAGTATTGCTGGTGTG	845
Query	910	TGGCCCAGG-CCTCTCCACGGCTGCAAGCTGGGGTGCAGGCTGTGGCTACCAACGGG	968
Sbjct	846	TAGCCC-GGACCTCACCCATGCTGTGCAACTGGGGTTCAGGCTGTGATCTATCATGGG	904
Query	969	GGCTATCTCCCTTCGGGACCCAAAC-AGCGAGGAGAACAGCAACGAATTGCCCTGGT	1027
Sbjct	905	GGCTACCTCCCTTCGAGACCTA-CTATCGACAAAAGCAATGACATTGCCCTGGT	963
Query	1028	CCACCTCTCCAG-TCCCTGCCCTCACAGAATACATCCAGCCTGTGCTCCAGCTG	1086

Sbjct	964	CCACCTCTAGCTCCC-TGCCTCTCACAGAATACATCCAGCCAGTGTGTCCTCGCTG	1022
Query	1087	CCGGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGCAACACCGAGT	1146
Sbjct	1023	CGGGACAGGCCCTGGTGGATGGCAAGGTCTGTACTGTGACCGCTGGGTAACACACAGT	1082
Query	1147	ACTATGGCAAACAGGCCGGGACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATG	1206
Sbjct	1083	TCTATGGCAAACAGGTATGGTGTCCAAGAGGCCGGTCCCATATAAGCAACGAAG	1142
Query	1207	TCTGCAATTGGCCTGACTCTATGGAAACAGATCAAGCCAAAGATGTTCTGTGCTGGCT	1266
Sbjct	1143	TTTGCAACAGCCCCGACTCTACGGGATCAGATCAAGCCAAAGATGTTCTGTGCTGGCT	1202
Query	1267	ACCCCGAGGGTGGCATTGATGCCAGGGCAGCGGTGGTCCCTTGTGTTGAGG	1326
Sbjct	1203	ATCCTGAGGGTGGCATTGATGCCAGGGCAGCTGGGATCAGATCAAGCCAAAGATGTTCTGTGCTGGCT	1262
Query	1327	ACAGCATCTCTGGCACGCCACGTTGGCGCTGTGTGGCATTGTGAGTTGGGACTGGCT	1386
Sbjct	1263	ACAGCATCTCTGGACATCAAGTGGCGGTATGTGGCATTTGTAAGCTGGGTACGGGCT	1322
Query	1387	GTCCTGGCCCAGAACGCCAGGCGTCTACACCAAAGTCAGTGACTTCCGGAGTGGATCT	1446
Sbjct	1323	GTGCTTGGGCCGGAAAGCCAGGAGTGTACACCAAAGTCAGTGACTTCCGGAGTGGATCT	1382
Query	1447	TCCAGGCCATAAAGACTCACTCGAAGCCAGCGCATGGTGACCCAGCTCTGA-CCGG--	1503
Sbjct	1383	TCAAGGCCATAAAGACTCACTCGAAGCCAGTGGCATGGTACTCAGCCCTGATCCGCC	1442
Query	1504	TGG-CT---T-CTC-G--CTGCGC-AGCCTCCAGGGCCCGAG--G-T--GAT--C-CC-G	1545
Sbjct	1443	TCATCTCGCTGCTCCGTGCTGCACTAGCATCCAGAGTCAGAGTTGGCTGGCTCCAG	1502
Query	1546	-----GTGGTGGGATCCACGCTGGGCG-AGGATGGGACGTTTTCTCTGGGCCGG	1598
Sbjct	1503	CCCCACGTGGTAGGCTCACACTGGCCTCAC-ATGGAATGGTTCCCTGCTCAGATCCAG	1561
Query	1599	TCCACAGGTTCAAGGACACCCCTCCCTCAGGGTCCCTCTTCCACAGTGGCGGGCCACT	1658
Sbjct	1562	TCCACGGGTTCAAGGATGC--TGGATCAAGGACTTCTCTTCCACAGTGGCGGGCCACT	1619
Query	1659	CAGCCCC-GAGACCACCCAAACCTCACCCCTCTGACCCCCATGTAATAATTGTTCTG-CTG	1716
Sbjct	1620	CAATCCCAGGG-CCATTGG-CCTCACCCCTCCC-ACCCC-ATGTAATAATTACTCTGTCC-	1674
Query	1717	TCTGGGACTC-CTGCTTAGGT-GCCCTGATGATGG-GATGCTCTTAAATAATAAGAT	1773
Sbjct	1675	TCTGGGGGGCGCT--CTAGGGAGCCCT--TG-TGCAGATGCTCTTAAATAATAAGGT	1729
Query	1774	GGTTTTGATT 1783	
Sbjct	1730	GGTTTGATT 1739	

>dbj|AK002694.1| Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610030A17 product:hepsin, full insert sequence
Length=1814

GENE ID: 15451 Hpn | hepsin [Mus musculus] (Over 10 PubMed links)

Score = 1181 bits (639), Expect = 0.0
Identities = 1275/1573 (81%), Gaps = 80/1573 (5%)
Strand=Plus/Plus

Query	259	AGGGTGGCGGACTG-TGCCATGCTGCTCCAGACCCAAAGTGGCAGCTCTCACTGCGGGG	317
Sbjct	274	AGGGTGGCGGACTGCACTGCTGCTCCAGACCCAAAGTGGCAGCTCTCATTGTGGGT	332
Query	318	ACCCGTACTT-CTGACAGCCATCGGGCGCGCATCTGGCCATTGTGGCTGTTCTCT	376
Sbjct	333	ACCCGTCT-GTTCTGACAGGCAATTGGGCGCGCTCTGGCCATTGTGACCATCCTACT	391
Query	377	-CAGGAGTGACCAAGGAGCCGCTGTACCGAGTGCAGGTCACT-CTGCGGACGCTCGGCTC	434
Sbjct	392	GCA-GAGTGACCAAGGAGCCACTGTACCAAGTGCAGCTCACT-TCCAGGGACTCACCGCTT	449
Query	435	ATGGTCTTGACAAGACGGAAGGG-ACGTGGCGCTGCTGTGCTCTCGCGCTCCAAACGC	493
Sbjct	450	GCGGTGTTGACAAGACGG-AGGGAACGTGGAGGCTACTGTGCTCTCACGCTCCAAATGC	508
Query	494	CAGGGTAGCCGGAACAGCTGCGAGGGAGATGGGCTTCCCTCAGGGCACTGACCCACTCCGA	553
Sbjct	509	CAGGGTAGCCGGAACAGCTGCGAGGGAGATGGGCTTCTCAGGGCTCTGGCGCACTCGGA	568
Query	554	GCTGGACGTGCGAACGGCGGGCGCAATGGCACGTGGCTGGCTCTCTGTGTTGGACGGAGGG	613
Sbjct	569	GCTGGATGTGCGCACTGCGGGCGCAACGGCACATCGGGCTTCTTGTGCGTGGACGA-GG	627
Query	614	GAGG-CTGCCCCACACCCAGAGGCTGCTGGAGGTCACTCCGTGTGATTGCCCCAGAG	672
Sbjct	628	GCGGACTGCCTCTGGCTCAGAGGTGCTGGATGTCATCTGTATGACTGTCCCTAGAG	687
Query	673	GCCGTTTCTGGCCGCCATCTGCCAAGACTGTGGCCAGGAAGCTGCCGTGGACCGCA	732
Sbjct	688	GCCGATTCTGACTGCCACCTGCCAAGACTGTGGCCGA-GAAGCTGCCGTGGACCGCA	746

Query	733	TCGTGGGAGGCCGGACACCAGCT-TGGGCCGGTGGCGTGGCAAGTCAGCCTTCGCTAT	791
Sbjct	747	TTGTGGGGGCCAGGACAGCAG-TCTGGGAAGGTGGCGTGGCAGGTCAAGCCTGCGTTAT	805
Query	792	GATGGAGCA-CACCTCTGTGGGGATCCCTGCTCTC-CGGGACTGGGTGCTGACAGCCG	849
Sbjct	806	GATGG-GTACCAACCTCTGTGGGGGT-CCTGCTGTCTC-GGGACTGGGTGCTGACTGCTG	862
Query	850	CCCACTGCTCCCGGAGC-GGA-ACCGGGTCTGTCCCAGTGCGAGTGGAGTGGTGC	907
Sbjct	863	CACATTGCTTCCAGAGCGGGAGA-C-GGTCTGTCTCGGTGGCGAGTATTTGCTGGTGC	920
Query	908	CGTGGCCAGG-CCTCTCCCCACGGTCTGCAGCTGGGGTGCAGGTGTTGCTACACAG	966
Sbjct	921	TGTAGGCC-GGACCTCACCCATGCTGTGCAACT-GGGGTTCAGGCTGTGATCTATCATG	978
Query	967	GGGGCTATCTTCC-CTTTCGGGACCCAAAC-AGCGAGGAGAACAGCAACGATATTGCCCT	1024
Sbjct	979	GGGGCTA-CCTCCTCTTCGAGA-CCCTACTATCGACGAAAACAGCAATGACATTGCC	1036
Query	1025	GGTCCAACCTCTCAGTC-CCCTGCCCTCACAGAATACTCCAGCCTGTGCGCTCCCAG	1083
Sbjct	1037	GGTCAAACCTCTCTAG-CTCCCTGCCCTCACAGAATACTCCAGCAGTGTGCTCCCTG	1095
Query	1084	CTGCCGGCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGCTGGGCAACACGC	1143
Sbjct	1096	CTGCCGGCAGGCCCTGGTGGATGGCAAGGTCTGTACTGTGACCGCTGGGTAACACAC	1155
Query	1144	AGTACTATGCCAAAGGCCGGTACTCCAGGAGGCTCGAGTCCCTATAATCAGCAATG	1203
Sbjct	1156	AGTTCTATGCCAAAGGGTATGGTCTCCAAAGAGGCCGGTCTCCATCATAAGCAACG	1215
Query	1204	ATGTCTGCAATGGCGCTGACTTCTATGAAACAGATCAAGCCAAAGATGTTCTGTGCTG	1263
Sbjct	1216	AAGTTGCAACAGCCCGACTCTACGGGAACTCAGATAAGCCAAAGATGTTCTGTGCTG	1275
Query	1264	GCTACCCCGAGGGTGGATTGATGCCCTGCCAGGGCGACAGCGGTGGTCCCTTGTGTTG	1323
Sbjct	1276	GCTATCCTGAGGTGGCATTGATGCGTGCCAGGGCGACAGTGGAGGCCCTTGTGTTG	1335
Query	1324	AGGACAGCATCTCTCGACGCCAGTGGCGCTGTGTGCGATTGTGAGTTGGGCACTG	1383
Sbjct	1336	AAGACAGCATCTCTGGGACATCAAGGTGGCGCTATGTGCGATTGTGAACTGGTACGG	1395
Query	1384	GCTGTGCCCTGGCCAGAACGCCAGCGTCTACACCAAAGTCAGTGAATTCCGGAGTGG	1443
Sbjct	1396	GCTGTGCTTGGCCGGAGGCCAGGAGTGTACACCAAAGTCAGTGAATTCCGGAGTGG	1455
Query	1444	TCTTCCAGGCCATAAAGACTCACTCCGAAGGCCAGCGCATGGTGACCCAGCTCTGA-CCG	1502
Sbjct	1456	TCTTCAAGGCCATAAAGACTCACTCCGAAGCCAGTGGCATGGTACCTGCCCTGATCCC	1515
Query	1503	G--TGG-CT---T-CTC-G--CTGCAGCAGCTCCAGGGCCCGAG--G-T--GAT--C-C	1543
Sbjct	1516	GCCTCATCTCGCTGCTCCGTGCTGCACTAGCATCCAGAGTCAGAGTGGCTGGTGGCTC	1575
Query	1544	C-G-----GTGGTGGGATCCACCGCTGGCGC-AGGATGGGACGTTTTCTTCTTGGGCC	1595
Sbjct	1576	CAGCCCCACGTGGTAGGCTCCACACTGGGCTCAC-ATGGAATGGTTCTGCTCAGATC	1634
Query	1596	CGGTCCACAGGTCCAAGGACACCCCTCCCTCCAGGGTCTCTCTTCCACAGTGGGGCCC	1655
Sbjct	1635	CAGTCCACGGGTCCAAGGATGC--TGGATCCAGGGACTTCTCTTCCACAGTGGGGCCC	1692
Query	1656	ACTCAGCCCC-GAGACCACCCACCTCACCCCTCTGACCCCATGTAATATTGTCTG-	1713
Sbjct	1693	ACTCAATCCCAGGG-CCATTGG-CCTCACCCCTCCC-ACCCC-ATGTAATATTACTCTGT	1748
Query	1714	CTGTCTGGGACTC-CTGTCTAGGT-GCCCTGATGATGG-GATGCTCTTAAATAATAAA	1770
Sbjct	1749	CC-TCTGGGGGGCGCT-CTAGGGAGCCCCT-TG-TGCAAGATGCTTTAAATAATAAA	1802
Query	1771	GATGGTTTGATT 1783	
Sbjct	1803	GGTGGTTTT-ATT 1814	

>ref|XM_512584.2| PREDICTED: Pan troglodytes hepsin (transmembrane protease, serine 1), transcript variant 3 (HPN), mRNA
Length=1572

GENE ID: 455944 HPN | hepsin (transmembrane protease, serine 1)
[Pan troglodytes]

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 1011 bits (547), Expect = 0.0
Identities = 549/550 (99%), Gaps = 0/550 (0%)
Strand=Plus/Plus

Query	658	GTGATTGCCAGAGGCCGTTCTGGCGCCATCTGCCAAGACTGTGGCCGCAGGAAGC	717
Sbjct	490	GTGATTGCCAGAGGCCGTTCTGGCGCCATCTGCCAAGACTGTGGCCGCAGGAAGC	549

Query	718	TGCCCCGTGGACCGCATCGTGGGAGGCCGGGACACCAGCTTGGGCCGTGGCAAG	777
Sbjct	550	TGCCCCGTGGACCGCATCGTGGGAGGCCGGGACACCAGCTTGGGCCGTGGCAAG	609
Query	778	TCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGGATCCCTGCTCTCGGGGACTGGG	837
Sbjct	610	TCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGGATCCCTGCTCTCGGGGACTGGG	669
Query	838	TGCTGA CAGCCGCCACTGCTTCCCAGGGAGCGGAACCGGGCTCTGTCCTGATGGCGAGTGT	897
Sbjct	670	TGCTGA CAGCCGCCACTGCTTCCCAGGGAGCGGAACCGGGCTCTGTCCTGATGGCGAGTGT	729
Query	898	TTGCCGGTGCCTGGCCAGGCCCTCTCCCCACGGCTCTGCACTGGGGTGCAGGCTGTGG	957
Sbjct	730	TTGCCGGTGCCTGGCCAGGCCCTCTCCCCACGGCTCTGCACTGGGGTGCAGGCTGTGG	789
Query	958	TCTACCA CGGGGGTATCTTCCCTTCGGGACCCAAACAGCAGGGAGAACAGCAACGATA	1017
Sbjct	790	TCTACCA CGGGGGTATCTTCCCTTCGGGACCCAAACAGCAGGGAGAACAGCAACGATA	849
Query	1018	TTGCCCTGGTCCACCTCTCCAGTCCCCCTCACAGAAATACATCCAGCCTGTGTGCC	1077
Sbjct	850	TTGCCCTGGTCCACCTCTCCAGTCCCCCTCACAGAAATACATCCAGCCTGTGTGCC	909
Query	1078	TCCCAGCTGCCGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGCTGGGCA	1137
Sbjct	910	TCCCAGCTGCCGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGCTGGGCA	969
Query	1138	ACACGCAGTACTATGGCAAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCA	1197
Sbjct	970	ACACGCAGTACTATGGCAAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCA	1029
Query	1198	GCAATGATGT 1207	
Sbjct	1030	GCAATGATGT 1039	

Score = 968 bits (524), Expect = 0.0
 Identities = 528/530 (99%), Gaps = 0/530 (0%)
 Strand=Plus/Plus

Query	1254	TTCTGTGCTGGCTA CCCCAGGGTGGCATTGATGCCCTGCCAGGGCGACAGCGGTGGTCCC	1313
Sbjct	1041	TTCTGTGCTGGCTA CCCCAGGGTGGCATTGATGCCCTGCCAGGGCGACAGCGGTGGTCCC	1100
Query	1314	TTTGTGTGAGGA CAGCATCTCTGGACGCCAGTTGGCGCTGTGTGGCATTGTGAGT	1373
Sbjct	1101	TTTGTGTGAGGA CAGCATCTCTGGACGCCAGTTGGCGCTGTGTGGCATTGTGAGT	1160
Query	1374	TGGGGCACTGGCTGTGCCCTGGCCCAGAACGCCAGGGCTACACCAAAGTCAGTGACTTC	1433
Sbjct	1161	TGGGGCACTGGCTGTGCCCTGGCCCAGAACGCCAGGGCTACACCAAAGTCAGTGACTTC	1220
Query	1434	CGGGAGTGGATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGGATGGTACCCAG	1493
Sbjct	1221	CGGGAGTGGATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGGATGGTACCCAG	1280
Query	1494	CTCTGACCGGTGGCTTCTCGCTCGCAGCCTCCAGGGCCGAGGTGATCCCGTGGTGG	1553
Sbjct	1281	CTCTGACCGGTGGCTTCTCGCTCGCAGCCTCCAGGGCCGAGGTGATCCCGTGGTGG	1340
Query	1554	ATCCACGCTGGCCAGGGATGGACGTTTTCTCTTGGGCCGGTCCACAGGTCCAAGG	1613
Sbjct	1341	ATCCACGCTGGCCAGGGATGGACGTTTTCTCTTGGGCCGGTCCACAGGTCCAAGG	1400
Query	1614	ACACCCCTCCCTCCAGGGTCTCTTCCACAGTGGGGCCCCACTCAGCCCCGAGACCAC	1673
Sbjct	1401	ACACCCCTCCCTCCAGGGTCTCTTCCACAGTGGGGCCCCACTCAGCCCCGAGACCAC	1460
Query	1674	CCAACCTCACCCCTCTGACCCCCATGTAATATTGTCTGCTGTCTGGACTCCTGTCTA	1733
Sbjct	1461	CCAACCTCACCCCTCTGACCCCCATGTAATATTGTCTGCTGTCTGGACTCCTGTCTA	1520
Query	1734	GGTGCCCTGATGATGGGATGCTTTAAATAATAAGATGGTTTGATT 1783	
Sbjct	1521	GGTGCCCTGATGACGGGATGCTTTAAATAATAAGATGGTTTGATT 1570	

Score = 638 bits (345), Expect = 3e-179
 Identities = 345/345 (100%), Gaps = 0/345 (0%)
 Strand=Plus/Plus

Query	191	GGTCCCACCTGGCCAGGGAGGTCA GCCAGGGATCATTAACAAGAGGCAGTGACATGGC	250
Sbjct	146	GGTCCCACCTGGCCAGGGAGGTCA GCCAGGGATCATTAACAAGAGGCAGTGACATGGC	205
Query	251	GCAGAAGGAGGGTGGCCGGACTGTGCCATGCTGCCAGACCCAAGGTGGCAGCTCTCAC	310
Sbjct	206	GCAGAAGGAGGGTGGCCGGACTGTGCCATGCTGCCAGACCCAAGGTGGCAGCTCTCAC	265
Query	311	TGCGGGGACCCCTGCTACTCTGACAGCCATCGGGCGGCATCCTGGCCATTGTGGCTGT	370
Sbjct	266	TGCGGGGACCCCTGCTACTCTGACAGCCATCGGGCGGCATCCTGGCCATTGTGGCTGT	325
Query	371	TCTCCTCAGGAGTGACCAGGAGCCGCTGTACCCAGTGCAGGTCA GCTCTGCGGACGCTCG	430
Sbjct	326	TCTCCTCAGGAGTGACCAGGAGCCGCTGTACCCAGTGCAGGTCA GCTCTGCGGACGCTCG	385

Query	431	GCTCATGGTCTTTGACAAGACGGAAGGGACGTGGCGGCTGCTGTGCTCCTCGCGCTCCAA	490
Sbjct	386	GCTCATGGTCTTTGACAAGACGGAAGGGACGTGGCGGCTGCTGTGCTCCTCGCGCTCCAA	445
Query	491	CGCCAGGGTAGCCGGACTCAGCTGCCAGGAGATGGGCTTCCTCAG	535
Sbjct	446	CGCCAGGGTAGCCGGACTCAGCTGCCAGGAGATGGGCTTCCTCAG	490

>gb|BC072688.1|  Rattus norvegicus hepsin, mRNA (cDNA clone MGC:91742 IMAGE:7098661), complete cds
Length=1580

GENE ID: 29135 Hpn | hepsin [Rattus norvegicus] (10 or fewer PubMed links)

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 935 bits (506), Expect = 0.0
Identities = 828/983 (84%), Gaps = 23/983 (2%)
Strand=Plus/Plus

Query	184	ACCCCAGGGTCCCACCCCTGGCCCAGGAGGTCAGCCAGGAAATCATTAAACAAGAGGCAGTG	243
Sbjct	27	ACCCCAGGGTCCGCCAACAGGTCAACCTGGAAATCATTAAACAAGAGTCCTCG	86
Query	244	ACATGGCGCAGAAGGGGGTGGCCGGACTGTGCCATGCTGCTCCAGACCCAAGGTGGCAG	303
Sbjct	87	ACAT-G-GC-GAAGGAGGGTGGCCGGACTGCCACCATGCTGTTCCAGACCCAAGGTGGCAG	143
Query	304	CTCTCACTGCGGGGACCTGCTACTTC-TGACAGCCATCGGGCGGCATCCTGGGCCATT	362
Sbjct	144	CTCTCACTGTGGGGACCTGCTG-TTCCTGACAGGCATTGGGCTGCGTCCTGGGCCATT	202
Query	363	GTGGCTGTTCTCCT-CAGGAGTGACCAGGAGCCGCTGTACCCAGTGCAGGTCACT-CTCTG	420
Sbjct	203	GTGACCATCTACTAC-GGAGTGACCAGGAGCCACTGTACCAAGTGCAGCTCAGTCCGG	261
Query	421	CGGACGCTGGCTCATGGTCTTTGACAAGACGGAAGGG-A-CGTGGGGCTGCTGTGCTCC	479
Sbjct	262	-GGACTCTGACTTTGGTGTGACAAGACAGA-GGGAACGTGGAGGCTGCTGTGCTCC	319
Query	480	TCGCGCTCCAACGCCAGGGTAGCCGGACTCAGCTGCAGGAGATGGGCTTCCTCAGGGCA	539
Sbjct	320	TCACGCTCCAACGCCAGGGTAGCAGGGCTCGGCTGTGAGGAGATGGCTTCTCAGGGCT	379
Query	540	CTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGGCCAATGGCACGTCGGGCTTC	599
Sbjct	380	CTGGCGCACTCAGAGCTGGATGTGCAACGCCAACGGCACATCGGGCTTC	439
Query	600	TGTGTGGACGAGGGGAGG-CTGCCCCAACCCAGAGGCTGCTGGAGGTATCTCCGTGTG	658
Sbjct	440	TGCGTGGACGAGGGC-GGTCTGCTCTGGCTCAGCGGTGCTGGATGTATCTCTGTATG	498
Query	659	TGATTGCCCCAGAGGCCGTTCTGGCGCATCTGCCAAGACTGTGGCGCAGGAAGCT	718
Sbjct	499	CGACTGTCTAGAGGCCGATTCTGACTGCCACCTGCCAAGACTGTGGCGCAGGAAGCT	558
Query	719	GCCCCTGGACCGCATCGTGGGAGGCCGGACACCAGCTGGCGGTGGCGTGGCAAGT	778
Sbjct	559	GCCGGTGGATCGCATTGGGGGGCCAGGACAGCAGCCTGGAAAGATGGCATGGCAGGT	618
Query	779	CAGCCTTCGCTATGATGG-AGCACACCTCTGTGGGGATCCCTGCTCTCGGGACTGG	837
Sbjct	619	CAGCCTCGCTTATGATGGGACC-CACCTCTGTGGGGATCCCTGCTGTCCGGGACTGG	677
Query	838	TGCTGACAGCCGCCACTGCTTCCCGGAGCGGAACCGGGCTCTGCTCCGATGGCAGTGT	897
Sbjct	678	TACTGACCGCTGCAACTGCTTCCAGAGAGGAACCGGGCTCTGCTCGGTGGCAGTAT	737
Query	898	TTGCCGGTGGCGCTGGCCAGG-CCTCTCCCAACGGTC-TGCAGCTGGGGTGCAGGCTGT	955
Sbjct	738	TTGCTGGTGCTGTAGCCC-GGACCTCACCTCATGC-CGTGAGCTGGGGTCAAGCTGT	795
Query	956	GGTCTACCAACGGGGCTATCTCCCTTCGGACCCAAAC-AGCGAGGAGAACAGCAACG	1014
Sbjct	796	GATCTATCATGGGGTACCTTCCTTCAGACCCCTA-CTATCGAGAAAACAGCAATG	854
Query	1015	ATATTGCCCTGGTCCACCTCTCCAG-TCCCTGCCCTCACAGAAATACATCCAGCCTGTG	1073
Sbjct	855	ACATTGCCCTGGTCCACCTCTAGCTCCC-TGCCTCTCACAGAAATACATCCAGCCTG	913
Query	1074	TGCCTCCCAAGCTGCCAGGCGCAGGGCCTGGTGGATGGCAAGATCTGACCGTGA	1133
Sbjct	914	TGTCTCCCTGCTGCCAGGCGCAGGGCCTGGTGGACGGCAAGGTCTGTACAGTGACCGCTGG	973
Query	1134	GGCAACACGCGAGTACTATGGCCA	1156
Sbjct	974	GGTAACACACAGTTCTATGGCCA	996

Score = 265 bits (143), Expect = 6e-67
Identities = 405/525 (77%), Gaps = 44/525 (8%)
Strand=Plus/Plus

Query 1291 GCCAGGGCGACAGCGGTGGTCCCTTGTGTGAGGACAGCATCTCTCGG-ACGCCACGT 1349

Sbjct	993	GCCAGGGTACAGCGGAGGCCCTTGTATGTGAGGACAGAACATCAAGA	1051
Query	1350	TGGCGGCTGTGTGGCATTTGTGAGTTGGGCAGTGGCTGTGCCCTGGCCAGAACAGGCCAGGC	1409
Sbjct	1052	TGGCGGCTGTGGCATTTGTAAAGCTGGGTCAGGGCTGTGCTTGGCCGGAAAGCCGGGA	1111
Query	1410	GTCTACACCAAAGTCAGTGACTTCGGGAGTGGATCTTCAGGCCATAAGACTCACTCC	1469
Sbjct	1112	GTGTACACCAAAGTCAGTGACTTCGGGAGTGGATCTTCAGGCCATAAGACTCACTCC	1171
Query	1470	GAAGCCAGGGCATGGTGACCCAGCTGTGACCG-G-TG-GCTT-CTC-GC-TGCGC	1519
Sbjct	1172	GAAGCTACCGGATGGTAACTCAGCCGTGACCCGCCATCGCCTGCTCCGCGCTGCTC	1231
Query	1520	-AGCCTCCAGGGCCGAG-G-T-GAT-C-CCGGT-G-GTGGGA-TCCACGCTG	1563
Sbjct	1232	CAGCATCCAGAGTCAGAGTTGGTCTGGTGGCTCCAGGCCACGTGGCAGGCTCACACTG	1291
Query	1564	GGCCG-AGGATGGGACGTTTTCTTCTGGGCCGGTCCACAGGTCCAAGGACACCCCTCC	1622
Sbjct	1292	GGCCTCAC-ATGGAACGGTTTCTGCTGGATCCAGTCCATAGATCCAAGGATGC-TGG	1348
Query	1623	CTCCAGGGTCTCTTCCACAGTGGGGGCCACTCAGCCCC-GAGACCACCAACCTC	1681
Sbjct	1349	GTCCAAGGACCTCTTCCACAGTGGCCGGCCACTCAATCCCAGGG-CCATTGG-CCTC	1406
Query	1682	ACCCCTCTGACCCCATGTAAATATTGTTCTG-CTGTCTGGGA-CTCCTGTCTAGGTGCC	1739
Sbjct	1407	ACCCCTCCC-ACCCC-ATGAAATATTACTCTGTCC-TCTGGGGCTCTTCGAGGCC	1463
Query	1740	CCTGATGATG-GGATGCTTTAAATAATAAGATGGTTTGATT	1783
Sbjct	1464	CCT--TG-TGGGATGCTTTAAATAATAAGGTGGTTTGATT	1505

>gb|AY234104.1| Mus musculus truncated hepsin splice variant mRNA, complete cds;
alternatively spliced
Length=1887

GENE ID: 15451 Hpn | hepsin [Mus musculus] (Over 10 PubMed links)

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 880 bits (476), Expect = 0.0
Identities = 944/1164 (81%), Gaps = 56/1164 (4%)
Strand=Plus/Plus
Query 658 GTGATTGCCAGAGGCCCTTCTGGCCGCATCTGCCAGACTGTGGCCGAGGAAGC 717
Sbjct 720 GTGACTGTCTAGAGGCCATTCTGACTGCCACCTGCCAGACTGTGGCCGAGGAAGC 779
Query 718 TGCCCGTGGACCGCATCGTGGGAGGCCGGACACCAG-CTTGGGCCGTGGCCCAA 776
Sbjct 780 TGCCGGTGGACCGCATGTGGGGGCCAGGACAGCAGTCT-GGAAAGTGGCCGTGGCAG 838
Query 777 GTCAGCCTTCGCTATGATGG-AGCACACCTCTGTGGGGATCCCTGCTCTCCGGGACTG 835
Sbjct 839 GTCAGCCTTCGCTATGATGGACC-CACCTCTGTGGGGTCCCTGCTCTCCGGGACTG 897
Query 836 GGTGCTGACAGCCGCCACTGCTCCGGAGCGGAACCGGGCTCTGTCCGATGGCGAGT 895
Sbjct 898 GGTGCTGACTGCTGACATTGCTTCCAGAGCGGAACCGGGCTCTGTCTCCGGGAGT 957
Query 896 GTTGCCGGTGGCCAGG-CCTCTCCCCACGGCTCTGCAGCTGGGGTGCAAGGCTG 954
Sbjct 958 ATTGCTGGCTGTAGCCC-GGACCTCACCCATGCTGCACTGGGGTTCAGGCTG 1016
Query 955 TGGTCTACACGGGGCTATCTCCCTTCGGGACCCCAAC-AGCGAGGAGAACAGCAAC 1013
Sbjct 1017 TGATCTATCATGGGGCTACCTCCCTTCGAGACCTA-CTATTGACAAAAACAGCAAT 1075
Query 1014 GATATTGCCCTGGCACCTCTCCAG-TCCCTGCCCTCACAGAACATCCAGCCTGT 1072
Sbjct 1076 GACATTGCCCTGGCACCTCTAGCTCCC-TGCCTCTCACAGAACATCCAGCAGT 1134
Query 1073 GTGCCCTCCAGCTGCCAGGCCAGGCCCTGGATGGCAAGATCTGTACCGTGACGGCTG 1132
Sbjct 1135 GTGTCTCCCTGCTGCCAGGCCCTGGATGGCAAGGTCTGTACTGTGACGGCTG 1194
Query 1133 GGGCAACACCGCAGTACTATGCCAACAGGCCGGGTAATCCAGGAGGCTCGAGTCCCCAT 1192
Sbjct 1195 GGGTAACACACAGTTCTATGCCAACAGGCTATGGCTCAAGAGGCCGGTCCCAT 1254
Query 1193 AATCAGCAATGATGCTGCAATGGCGCTGACTCTATGAAACCAAGATCAAGCCCAAGAT 1252
Sbjct 1255 CATAAGCAACGAAGTTGCAACAGCCCCGACTTCTACGGGAATCAGATCAAGCCCAAGAT 1314
Query 1253 GTTCTGTGCTGGCTACCCGAGGGTGGCATTTGATGCTGCTGCCAGGGCAAGCGGTGGTCC 1312
Sbjct 1315 GTTCTGTGCTGGCTATCTGAGGGTGGCATTTGATGCTGCTGCCAGGGCAAGTGGAGGCC 1374
Query 1313 CTTTGTCTGGAGGACAGCATCTCGGACGCCACGTTGGCCGGCTGTGCTGGCATTGTGAG 1372
Sbjct 1375 CTTTGTCTGGAGGACAGCATCTCGGACATCAAGGTGGCGCTATGTGGCATTGTGAG 1434

Query	1373	TTGGGGCACTGGCTGTGCCCTGGCCAGAAGCCAGGCGTACACCAAAGTCAGTGACTT	1432
Sbjct	1435	CTGGGGTACCGGCTGTGCTTGGCCCGAAGCCAGGAGTGTACACCAAAGTCACTGACTT	1494
Query	1433	CCGGGAGTGGATCTCCAGGCCATAAGACTCACTCCGAAGCCAGGGCATGGTGACCCA	1492
Sbjct	1495	CCGGGAGTGGATCTCAAGGCCATAAGACTCACTCCGAAGCCAGTGGCATGGTGACTCA	1554
Query	1493	GCTCTGA-CGGG-TGG-CT--T-CTC-G-CTGCGC-AGCCTCCAGGGCCGAG--G-	1537
Sbjct	1555	GCCCTGATCCCGCCATCTCGCTGCTCGTGCAGTCAGCATCCAGAGTCAGAGTTGG	1614
Query	1538	T--GAT--C-CC-G-----GTGGTGGGATCCACGCTGGCCG-AGGATGGGACGTTTT	1584
Sbjct	1615	TCTGGTGGCTCCAGCCCCACGTGGTAGGCTCCACACTGGGCTCAC-ATGGAATGGTTTC	1673
Query	1585	CTTCTTGGGCCGGTCCACAGGTCCAAGGACACCCTCCCTCCAGGGCTCTCTTCCACA	1644
Sbjct	1674	CTGCTCAGATCCACAGGTCCAAGGATGC-TGGATCCAAGGACTCTCTTCCACA	1731
Query	1645	GTGGCGGGCCCACCTCAGCCCC-GAGACCAACCTCACCCCTTGACCCCCATGTAAA	1703
Sbjct	1732	GTGGCGGCCACCTCAATCCCAGGG-CCATTGG-CCTCACCCCTCCC-ACCCC-ATGTAAA	1787
Query	1704	TATTGTTCTG-CTGCTGGGACTC-CTGCTAGGT-GCCCTGATGATGG-GATGCTCTT	1759
Sbjct	1788	TATTACTCTGTCC-TCTGGGGGGCGCT-CTAGGGAGCCCT-TG-TGCAGATGCTCTT	1841
Query	1760	TAAATAATAAAGATGGTTTGATT 1783	
Sbjct	1842	TAAATAATAAAGGTGGTTTGATT 1865	

Score = 403 bits (218), Expect = 1e-108
 Identities = 394/477 (82%), Gaps = 19/477 (3%)
 Strand=Plus/Plus

Query	184	ACCCCAGGGTCCCACCCCTGGCCAGGAGGTAGCCAGGGAACTTAAACAAGAGGCAGTG	243
Sbjct	143	ACCCCAGGGTCCGCCAGGCCAACAGGTCAACCTGGGAACTTAAACAAGAGTCCTG	202
Query	244	ACATGGCGCAGAAGGAGGGTGGCCGGACTG-TGCCATGCTGCTCCAGACCCAAGGTGGCA	302
Sbjct	203	ACAT-G-GC-GAAGGAGGGTGGCCGGACTGCAG-CATGCTGCTCCAGACCCAAGGTGGCA	258
Query	303	GCTCTCACTGCGGGGACCCCTGCTACTTC-TGACAGCCATGGGGCGGCATCCCTGGCCAT	361
Sbjct	259	GCTCTCATTGGGTACCCCTGCT-TTCTGACAGGCATTGGGGCGCGTCTGGCCAT	317
Query	362	TGTGGCTGTTCTCCT-CAGGAGTGACCAGGAGCCGCTGTACCCAGTGCAGGTAGCTCT-	419
Sbjct	318	TGTGACCATCCTACTGCAG-AGTGACCAAGGAGCCACTGTACCAAGTGCAGCTCAG-TCCA	375
Query	420	GCGGACGCTGGCT-CATGGTCTTGTACAAGACGGAAGGG-ACGTGGCGCTGCTGTGC	476
Sbjct	376	GGGGACTCACGACTTGCAG-G-TGTTGGACAAGACGGA-GGGTACGTGGAGGCTACTGTGC	432
Query	477	TCCTCGCGCTCCAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGATGGCTTCCCTAGG	536
Sbjct	433	TCCTCACGCTCCAATGCCAGGGTGGCAGGGCTGGCTGTGAGGAGATGGCTTCTCAGG	492
Query	537	GCAC TGACCCACTCCGAGCTGGACGTGCGAACGGCGGCCAATGGCACGTGGCTTC	596
Sbjct	493	GCTCTGGCGACTCGGAGCTGGATGTGGCACTGCGGGCGCCAACGGCACATCGGGCTTC	552
Query	597	TTCTGTGTGGACGAGGGGAGG-CTGCCCCACACCCAGAGGCTGCTGGAGGTCATCTC	652
Sbjct	553	TTTTCGTGGACGAGGGC-GGACTGCCTCTGGCTCAGAGGTTGCTGGATGTCACTC	608

>ref|XM_001254640.1| PREDICTED: Bos taurus similar to hepsin (LOC787164), partial mRNA Length=779

GENE ID: 787164 LOC787164 | similar to hepsin [Bos taurus]

Score = 815 bits (441), Expect = 0.0
 Identities = 662/761 (86%), Gaps = 46/761 (6%)
 Strand=Plus/Plus

Query	1052	CACAGAAATACATCCAGCTGTGTGCCCTCCAGCTGCCGGCCAGGCCCTGGTGGATGGCAA	1111
Sbjct	34	CACAGAGTACATCCAGCCCGTGTCTCCCGCTGCCGGCAGGCCCTGGTGGATGGCAA	93
Query	1112	GATCTGTACCGTGACGGCTGGGCAACACGCACTGACTATGGCCAACAGGCCGGGTACT	1171
Sbjct	94	GATCTGCACGGTGACTGGCTGGGCAACACGCACTGACTACGCCAACAGGCTGGGTGCT	153
Query	1172	CCAGGAGGCTCGAGTCCCATAATCAGCAATGATGTCCTGCAATGGGCTGACTTCTATGG	1231
Sbjct	154	CCAGGAGGCCAGTCCCATAATCAGCAATGATGTCCTGCAACGCCCGACTTCTACGG	213
Query	1232	AAACCAAGATCAAGCCAAAGATGTTCTGTGCTGGCTACCCGAGGGTGGCATTGATGCCTG	1291
Sbjct	214	GAACCAAGATCAAGCCAAAGATGTTCTGTGCTGGCTACCCGAGGGTGGCATTGATGCCTG	273

Query	1292	CCAGGGCGACAGCGGTGGTCCCCTTGTGTGAGGACAGCATCTCTCGGACGCCACGTTG	1351
Sbjct	274	CCAGGGCGACAGTGGTGGCCCTTCGTGTGAGGATAGCATCTCTCGGACGCCACGTTG	333
Query	1352	GCGGCTGTGGCATTGTGAGTTGGGCACTGGCTGTGCCCTGGCCAGAAGCCAGGGT	1411
Sbjct	334	GCGGCTGTGGCATTGTGAGCTGGGCACCGGCTGTGCCCTGGCCAGAAGCCAGGGT	393
Query	1412	CTACACCAAAGTCAGTGAATTCCGGAGTGGATCTTCAAGGCCATAAGACTCACTCCGA	1471
Sbjct	394	CTACACCAAAGTCAGTGAATTCCGGAGTGGATCTTCAAGGCCATAAGACTCACTCCGA	453
Query	1472	AGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTC---GCTGCGCA-GCCTCCA	1527
Sbjct	454	AGCCAGCGGCATGGTAACCCAGCTTGACCTGTGGCTTCCTCGCTGTCACGCCCTCCA	513
Query	1528	GGGCCCGAGGTGATC-----CC----G-----GTGGTGGGATCCACGCTGGCCGAGG	1571
Sbjct	514	GGGCCCGAGCTGATCTAAGGGCCCCAGCCCCACGTGATGGGTTACCCCTGGGCG-AGG	572
Query	1572	-ATGGGACGTTTTCTTCTTGGGCCGGTCCACAGGTCCAAGGACACCC-CCCTCCAGG	1629
Sbjct	573	GATGGAACATTTTCTTCTTGGGCCAGCCCCACAGGTCCAAGGAACTCTTCCCTCCAAG	632
Query	1630	GTCCTCTCTTCCACAGTGGCGGGCCACTCAGCCCCAGACCAACCTCACCCCTCCT	1689
Sbjct	633	GTCCTC-C---ACAGTGGCGGGCCACTCAGCCCTGGGACCAACCC---TC-C---TGC-	679
Query	1690	GACCCCCATGTAATATTGTTCTGCTGTCTGGGA-CTCTG-----TCTAGGTGCCCC	1742
Sbjct	680	--CCCCATGTAATATTGTTCTGCCATCTGGATCCCCCCCCCATCTTG-TGCTCCT	736
Query	1743	GATGATGGGATGCTCTTAAATAATAAAGATGGTTTGATT	1783
Sbjct	737	GAAGACAGGATGCTCTTAAATAATAAAGATGGTTTGATT	777

>gb|BC119448.1| Mus musculus cDNA clone IMAGE:40044314
Length=772

Score = 717 bits (388), Expect = 0.0
Identities = 633/752 (84%), Gaps = 14/752 (1%)
Strand=Plus/Minus

Query	448	AGACGGAAAGGG-ACGTGGCGCTGCTGTGCTCCTCGCGCTCCAAACGCCAGGGTAGCCGGA	506
Sbjct	761	AGA-GGATGGGAACTGGAGGCTACTGTGCTCCTCACCGCTCCAAATGCCAGGGTGGCAGGG	703
Query	507	CTCAGCTGCGAGGAGATGGGCTTCCTCAGGGACTGACCCACTCCGAGCTGGACGTGCGA	566
Sbjct	702	CTCGGCTGTGAGGAGATGGGCTTCCTCAGGGCTCTGGCACACTCGGAGCTGGATGTGCGC	643
Query	567	ACGGCGGGGCCAATGCCACGTCGGCTTCTCTGTGTGACGAGGGAGG-CTGCCCA	625
Sbjct	642	ACTGCGGGGCCAACGGCACATCGGCTTCTTTCGCGTGGACGA-GGGCGACTGCCCT	584
Query	626	CACCCAGAGGCTGCTGGAGGTATCTCCGTGTGATTGCCAGAGGCCGTTCTTGGC	685
Sbjct	583	GGCTCAGAGGTTGCTGGATGTATCTCTGTATGTGACTGCTCTAGAGGCCATTCTGAC	524
Query	686	CGCCATCTGCCAAGACTGTGGCCGAGGAAGCTGCCGTGGACCGCATCGTGGAGGCCG	745
Sbjct	523	TGCCACCTGCCAAGACTGTGGCCGAGGAAGCTGCCGTGGACCGCATGTGGGGGCCA	464
Query	746	GGACACCAAG-CTTGGGCCGGTGGCGTGGCAAGTCAAGCCTTCGCTATGATGG-AGCACAC	803
Sbjct	463	GGACAGCAGTCT-GGGAGGTGGCCGTGGCAGGTCAAGCCTGCGTTATGATGGGACC-CAC	406
Query	804	CTCTGTGGGGATCCCTGCTCTCCGGGACTGGGTGCTGACAGCCGCCACTGCTTCCCG	863
Sbjct	405	CTCTGTGGGGTCCCTGCTGTCTGGGACTGGGTGCTGACTGCTGCACATTGCTTCCA	346
Query	864	GAGCGGAACCGGGTCTGTCCCAGTGGCGAGTGGTGGCGCTGGCCAGG-CCTC	922
Sbjct	345	GAGCGGAACCGGGTCTGTCTGGTGGCAGTATTTGCTGGTGTAGCCC-GGACCTC	287
Query	923	TCCCCACGGCTGCACTGGGGTGCAGGCTGTGGCTACACGGGCTATCTTCCCTT	982
Sbjct	286	ACCCCATGCTGTGCACTGGGGTCAAGGCTGTGATCTATCATGGGCTACCTTCCCTT	227
Query	983	TCGGGACCCAAAC-AGCGAGGAGAACAGCAACGATATTGCCCTGGTCCACCTCTCCAG-T	1040
Sbjct	226	TCGAGACCTA-CTATCGACAAAACAGCAATGACATTGCCCTGGTCCACCTCTCTAGCT	168
Query	1041	CCCCCTGCCCTCACAGAAATACATCCAGCCTGTGTGCTCCAGCTGCCGCCAGGCCCTG	1100
Sbjct	167	CCC-TGCGCTCTCACAGAAATACATCCAGCCAGTGTCTCCCTGCTGCCAGGCCCTG	109
Query	1101	GTGGATGGCAAGATCTGTACCGTGACGGCTGGGCAACACGCAGTACTATGGCAACAG	1160
Sbjct	108	GTGGATGGCAAGGTCTGTACTGTGACGGCTGGGTAACACACAGTTATGGCAACAG	49
Query	1161	GCCGGGGTACTCCAGGAGGCTCGAGTCCCCAT	1192
Sbjct	48	GCTATGGTGTCCAAGAGGCCGGTCCCCAT	17

>gb|BC119449.1| Mus musculus cDNA clone IMAGE:40044315

Length=772

Score = 712 bits (385), Expect = 0.0
 Identities = 632/752 (84%), Gaps = 14/752 (1%)
 Strand=Plus/Minus

Query 448	AGACGGAAGGG-ACGTGGCGCTGCTGTGCTCCTCGCGCTCCAAACGCCAGGGTAGCCGGA	506
Sbjct 761	AGA-GGATGGGAAACGTGGAGGCTACTGTGCTCCTCACGCTCCAATGCCAGGGTGGCAGGG	703
Query 507	CTCAGCTGCAGGAATGGCTTCCTCAGGGACTGACCCACTCCGAGCTGGACCTGCGA	566
Sbjct 702	CTCGGCTGTGAGGAGATGGCTTCAGGGCTCTGGCACACTCGGAGCTGGATGTGCGC	643
Query 567	ACGGCGGGGCCAATGGCACGTGGCGCTTCTCTGTGAGGAGGGAGG-CTGCCCA	625
Sbjct 642	ACTGCGGGGCCAATGGCACATGGCTTCCTTACGTGGACGA-GGGGGACTGCTCT	584
Query 626	CACCCAGAGGCTGCTGGAGGTATCTCCGTGTGATTGCCAGAGGCCGTTCTGGC	685
Sbjct 583	GGCTCAGAGGTTGCTGGATGTATCTGTATGTACTGCTCTAGAGGCCGATTCTGAC	524
Query 686	CGCCATCTGCCAACAGACTGTGGCGCAGGAAGCTGCCGTGGACCACATGTGGAGGCCG	745
Sbjct 523	TGCCACCTGCCAACAGACTGTGGCGCAGGAAGCTGCCGTGGACCACATTGTGGGGGCCA	464
Query 746	GGACACCAAG-CTTGGGCGGTGGCGTGGCAAGTCAGCCTCGCTATGATGG-AGCACAC	803
Sbjct 463	GGACAGCAGTCT-GGGAGGTGGCGTGGCAGGTAGCCTGCGTTATGATGGGACC-CAC	406
Query 804	CTCTGTGGGGATCCCTGCTCTCGGGACTGGGTGCTGACAGCCGCCACTGCTTCCG	863
Sbjct 405	CTCTGTGGGGGTCCTGCTGTCTGGGACTGGGTGCTGACTGCTGCACATTGCTTCCA	346
Query 864	GAGCGGAACCGGGTCTGTCCCAGTGGCGAGTGTTGCCGGTGCCGTGGCCAGG-CCTC	922
Sbjct 345	GAGCGGAACCGGGTCTGTCCCAGTGGCGAGTATTGCTGGTGCTGAGCCC-GGACCTC	287
Query 923	TCCCCACGGTCTGCAGCTGGGGTGCAAGGCTGTGGCTACCACGGGGCTATCTCCCTT	982
Sbjct 286	ACCCCATGCTGTGCAACTGGGGTTCAGGCTGTGATCTATCATGGGGCTACCTTCCCTT	227
Query 983	TCGGGACCCAAAC-AGCGAGGAGAACAGCAACGATATTGCCCTGGTCCACCTCTCAG-T	1040
Sbjct 226	TCGAGACCTA-CTATCGACAAAACAGCAATGACATTGCCCTGGTCCACCTCTAGCT	168
Query 1041	CCCCCTGCCCTCACAGAACATCCAGCCTGTGCTCCAGCTGCCGGCAGGCCCTG	1100
Sbjct 167	CCC-TGCCTCTCACAGAACATCCAGCAGTGTCTCCCTGCTGGGACAGGCCCTG	109
Query 1101	GTGGATGGCAAGATCTGTACCGTGACGGCTGGGCAACACGCAGTACTATGCCAACAG	1160
Sbjct 108	GTGGATGGCAAGGTCTGTACTGTGACCGGCTGGGTAACACACAGTTCTATGCCAACAG	49
Query 1161	GCCGGGGTACTCCAGGAGGCTCGAGTCCCCAT	1192
Sbjct 48	GCTATGGTGTCTCAAGAGGCCGGTCCCCAT	17

>gb|AC192150.4| Pan troglodytes BAC clone CH251-522E19 from chromosome 19, complete sequence
 Length=213011

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position

Score = 590 bits (319), Expect = 9e-165
Identities = 323/325 (99%), Gaps = 0/325 (0%)
Strand=Plus/Plus
Query 1459 AGACTCACTCGAACGCCAGCGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCG 1518
Sbjct 179133 AGACTCACTCGAACGCCAGCGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCG 179192
Query 1519 CAGCCTCCAGGGCCCGAGGTGATCCGGTGGTGGATCCACGCTGGGCCAGGATGGGAC 1578
Sbjct 179193 CAGCCTCCAGGGCCCGAGGTGATCCGGTGGATCCACGCTGGGCCAGGATGGGAC 179252
Query 1579 GTTTTTCTTCTGGGCCGCTCACAGGTCAAAGGACACCCCTCCCTCCAGGGTCTCTCT 1638
Sbjct 179253 GTTTTTCTTCTGGGCCGCTCACAGGTCAAAGGACACCCCTCCCTCCAGGGTCTCTCT 179312
Query 1639 TCCACAGTGGCGGGCCACTCAGGCCAGACCCAAACCTCACCTCCCTGACCCCCCAT 1698
Sbjct 179313 TCCACAGTGGCGGGCCACTCAGGCCAGACCCAAACCTCACCTCCCTGACCCCCCAT 179372
Query 1699 GTAAAAATTGTTCTGCTGTCTGGACTCCTGTCTAGGTGCCCTGATGATGGGATGCTCT 1758
Sbjct 179373 GTAAAAATTGTTCTGCTGTCTGGACTCCTGTCTAGGTGCCCTGATGACGGGATGCTCT 179432
Query 1759 TTAAAAATAAAAGATGGTTTGATT 1783
Sbjct 179433 TTAAAAATAAAAGATGGTTTGATT 179457

Score = 348 bits (188), Expect = 6e-92

Identities = 198/202 (98%), Gaps = 3/202 (1%)
 Strand=Plus/Plus

Query 858	TTCCC-GG-A-GCGGAACGGGTCCCTGTCCCGATGGCGAGTGTGTTGCCGGTGCGTGGCC	914
Sbjct 173569	TTCCCTGGTAGGCAGAACGGGTCCCTGTCCCGATGGCGAGTGTGTTGCCGGTGCGTGGCC	173628
Query 915	CAGGCCTCTCCCCACGGTCTGCAGCTGGGGTGCAGGCTGTGGCTACACGGGGCTAT	974
Sbjct 173629	CAGGCCTCTCCCCACGGCCTGCAGCTGGGGTGCAGGCTGTGGCTACACGGGGCTAT	173688
Query 975	CTTCCTTCGGGACCCAAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCACCTC	1034
Sbjct 173689	CTTCCTTCGGGACCCAAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCACCTC	173748
Query 1035	TCCAGTCCCCCTGCCCTCACAG 1056	
Sbjct 173749	TCCAGTCCCCCTGCCCTCACAG 173770	

Score = 315 bits (170), Expect = 6e-82
 Identities = 172/173 (99%), Gaps = 0/173 (0%)
 Strand=Plus/Plus

Query 1288	CCTGCCAGGGCGACAGCGGTGGTCCCTTGTGTGAGGACAGCATCTCGAACGCCAC	1347
Sbjct 178746	CCTCCCAGGGCGACAGCGGTGGTCCCTTGTGTGAGGACAGCATCTCGAACGCCAC	178805
Query 1348	GTTGGCGGCTGTGTGGCATTGTGAGTTGGGCACTGGCTGTGCCCTGGCCAGAACCCAG	1407
Sbjct 178806	GTTGGCGGCTGTGTGGCATTGTGAGTTGGGCACTGGCTGTGCCCTGGCCAGAACCCAG	178865
Query 1408	GCGTCTACACCAAAGTCAGTGACTTCCGGAGTGAGATCTCCAGGCCATAAAG 1460	
Sbjct 178866	GCGTCTACACCAAAGTCAGTGACTTCCGGAGTGAGATCTCCAGGCCATAAAG 178918	

Score = 313 bits (169), Expect = 2e-81
 Identities = 172/173 (99%), Gaps = 1/173 (0%)
 Strand=Plus/Plus

Query 695	CCA-AGACTGTGGCCGCAGGAAGCTGCCGTGGACCGCATCGTGGAGGCCGGACACCA	753
Sbjct 173295	CCACAGACTGTGGCCGCAGGAAGCTGCCGTGGACCGCATCGTGGAGGCCGGACACCA	173354
Query 754	GCTTGGGCCGGTGGCGTGGCAAGTCAGCCTCGCTATGATGGAGCACACCTGTGGGG	813
Sbjct 173355	GCTTGGGCCGGTGGCGTGGCAAGTCAGCCTCGCTATGATGGAGCACACCTGTGGGG	173414
Query 814	GATCCCTGCTCTCGGGGACTGGTGCTGACAGCCGCCACTGCTTCCGGAG 866	
Sbjct 173415	GATCCCTGCTCTCGGGGACTGGTGCTGACAGCCGCCACTGCTTCCGGAG 173467	

Score = 289 bits (156), Expect = 4e-74
 Identities = 156/156 (100%), Gaps = 0/156 (0%)
 Strand=Plus/Plus

Query 38	CAGGTGAGGCAGCCTGGCCTAGCAGGCCACGCCCTCTGCCCTCAGGCCGCCCG	97
Sbjct 154680	CAGGTGAGGCAGCCTGGCCTAGCAGGCCACGCCCTCTGCCCTCAGGCCGCCCG	154739
Query 98	CTGCTGGGGGCCACCATGCTCCTGCCAGGCCTGGAGACTGACCCGACCCGGCACTAC	157
Sbjct 154740	CTGCTGGGGGCCACCATGCTCCTGCCAGGCCTGGAGACTGACCCGACCCGGCACTAC	154799
Query 158	CTCGAGGCTCGCCCCCACCTGCTGGACCCCAAGGGT 193	
Sbjct 154800	CTCGAGGCTCGCCCCCACCTGCTGGACCCCAAGGGT 154835	

Score = 268 bits (145), Expect = 5e-68
 Identities = 145/145 (100%), Gaps = 0/145 (0%)
 Strand=Plus/Plus

Query 1152	GGCCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGC	1211
Sbjct 178425	GGCCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGC	178484
Query 1212	AATGGCGCTGACTTCTATGAAACAGATCAAGCCAAGATGTTCTGTGCTGGCTACCC	1271
Sbjct 178485	AATGGCGCTGACTTCTATGAAACAGATCAAGCCAAGATGTTCTGTGCTGGCTACCC	178544
Query 1272	GAGGGTGGCATTGATGCCCTGCCAGG 1296	
Sbjct 178545	GAGGGTGGCATTGATGCCCTGCCAGG 178569	

Score = 248 bits (134), Expect = 6e-62
 Identities = 134/134 (100%), Gaps = 0/134 (0%)
 Strand=Plus/Plus

Query 403	CAGTGCAGGTCACTCTGCCAGCTCGGCCATGGCTTTGACAAGACGGAAAGGGACGT	462
Sbjct 172624	CAGTGCAGGTCACTCTGCCAGCTCGGCCATGGCTTTGACAAGACGGAAAGGGACGT	172683
Query 463	GGCGGGCTGCTGTGCTCTCGCGCTCAACGCCAGGGTAGCCGACTCAGCTGGAGGAGA	522

Sbjct 172684 GGCGGCTGCTGTGCTCCTCGCGTCCAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGA 172743
 Query 523 TGGGCTTCCTCAGG 536
 Sbjct 172744 TGGGCTTCCTCAGG 172757

Score = 228 bits (123), Expect = 8e-56
 Identities = 128/130 (98%), Gaps = 1/130 (0%)
 Strand=Plus/Plus

Query 533 CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCCAATGGCACGTCGG 592
 Sbjct 172825 CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCCAATGGCACGTCGG 172884

Query 593 CTTCTTCTGTGTGGACGAGGGGAGGGCTGCCACACCCAGAGGGCTGCTGGAGGTCTCATCTC 652
 Sbjct 172885 CTTCTTCTGCCTGGACGAGGGGAGGGCTGCCACACCCAGAGGGCTGCTGGAGGTCTCATCTC 172944

Query 653 CGTGTG-TGA 661
 Sbjct 172945 CGTGTGGTGA 172954

Score = 191 bits (103), Expect = 1e-44
 Identities = 103/103 (100%), Gaps = 0/103 (0%)
 Strand=Plus/Plus

Query 261 GGTGGCCGGACTGTGCCATGCTGCCAGACCCAAAGGTGGCAGCTCTCACTGCGGGGACC 320
 Sbjct 162138 GGTGGCCGGACTGTGCCATGCTGCCAGACCCAAAGGTGGCAGCTCTCACTGCGGGGACC 162197

Query 321 CTGCTACTTCTGACAGCCATCGGGCGGCATCCTGGGCCATTG 363
 Sbjct 162198 CTGCTACTTCTGACAGCCATCGGGCGGCATCCTGGGCCATTG 162240

Score = 189 bits (102), Expect = 4e-44
 Identities = 102/102 (100%), Gaps = 0/102 (0%)
 Strand=Plus/Plus

Query 1052 CACAGAAATACATCCAGCCCTGTGTGCTCTCCAGCTGCCGCCAGGCCCTGGTGATGGCAA 1111
 Sbjct 178132 CACAGAAATACATCCAGCCCTGTGTGCTCTCCAGCTGCCGCCAGGCCCTGGTGATGGCAA 178191

Query 1112 GATCTGTACCGTGACGGGCTGGGGCAACACGCAGTACTATGG 1153
 Sbjct 178192 GATCTGTACCGTGACGGGCTGGGGCAACACGCAGTACTATGG 178233

Score = 137 bits (74), Expect = 1e-28
 Identities = 74/74 (100%), Gaps = 0/74 (0%)
 Strand=Plus/Plus

Query 191 GGTCCCACCCCTGGCCAGGGAGGTCAAGCCAGGGAAATCATTAAACAAGAGGCAGTGACATGGC 250
 Sbjct 155413 GGTCCCACCCCTGGCCAGGGAGGTCAAGCCAGGGAAATCATTAAACAAGAGGCAGTGACATGGC 155472

Query 251 GCAGAAGGAGGGTG 264
 Sbjct 155473 GCAGAAGGAGGGTG 155486

Score = 80.5 bits (43), Expect = 2e-11
 Identities = 43/43 (100%), Gaps = 0/43 (0%)
 Strand=Plus/Plus

Query 363 GTGGCTGTTCTCTCAGGAGTGACCAAGGAGCCGCTGTACCCAG 405
 Sbjct 162323 GTGGCTGTTCTCTCAGGAGTGACCAAGGAGCCGCTGTACCCAG 162365

Score = 78.7 bits (42), Expect = 9e-11
 Identities = 42/42 (100%), Gaps = 0/42 (0%)
 Strand=Plus/Plus

Query 658 GTGATTGCCAGAGGCCGTTCTGGCCGCCATCTGCCAAG 699
 Sbjct 173082 GTGATTGCCAGAGGCCGTTCTGGCCGCCATCTGCCAAG 173123

>dbj|AK091988.1| Homo sapiens cDNA FLJ34669 fis, clone LIVER2001051
 Length=2547

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position

Score = 590 bits (319), Expect = 9e-165
 Identities = 323/325 (99%), Gaps = 0/325 (0%)
 Strand=Plus/Plus

Query 1459 AGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCG 1518
 Sbjct 2223 AGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTTCTCGCTGCG 2282

Query 1519 CAGCCTCCAGGGCCCGAGGTGATCCGGTGGATCCACGCTGGCCGAGGATGGGAC 1578

Sbjct	2283	CAGCCTCCAGGGCCGAGGTGATCCCCTGGTGGGATCCACGCTGGCCTAGGATGGGAC	2342
Query	1579	GTTTTCTCTGGGCCGGTCCACAGGTCAAGGACACCCCTCCCTCAGGGTCCTCTCT	1638
Sbjct	2343	GTTTTCTCTGGGCCGGTCCACAGGTCAAGGACACCCCTCCCTCAGGGTCCTCTCT	2402
Query	1639	TCCACAGTGCGGGCCCACTCAGCCCCGAGACCACCAACCTCACCCCTGACCCCCAT	1698
Sbjct	2403	TCCACAGTGCGGGCCCACTCAGCCCCGAGACCACCAACCTCACCCCTGACCCCCAT	2462
Query	1699	GTAAATATTGTTCTGCTGTCTGGACTCCCTGTCTAGGTGCCCTGATGATGGGATGCTCT	1758
Sbjct	2463	GTAAATATTGTTCTGCTGTCTGGACTCCCTGTCTAGGTGCCCTGATGACGGGATGCTCT	2522
Query	1759	TTAATAATAAGATGGTTTGATT	1783
Sbjct	2523	TTAATAATAAGATGGTTTGATT	2547

Score = 315 bits (170), Expect = 6e-82
 Identities = 172/173 (99%), Gaps = 0/173 (0%)
 Strand=Plus/Plus

Query	1288	CCTGCCAGGGCGACAGCGGTGGTCCCTTGTGTGAGGACAGCATCTCTGGACGCCAC	1347
Sbjct	1836	CCTCCCAGGGCGACAGCGGTGGTCCCTTGTGTGAGGACAGCATCTCTGGACGCCAC	1895
Query	1348	GTTGGCGGTGTGTGGCATTGTGAGTTGGGCACTGGCTGTGCCCTGGCCAGAACCCAG	1407
Sbjct	1896	GTTGGCGGTGTGTGGCATTGTGAGTTGGGCACTGGCTGTGCCCTGGCCAGAACCCAG	1955
Query	1408	GCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTCCAGGGCATAAAG	1460
Sbjct	1956	GCGTCTACACCAAAGTCAGTGACTTCCGGGAGTGGATCTCCAGGGCATAAAG	2008

Score = 268 bits (145), Expect = 5e-68
 Identities = 145/145 (100%), Gaps = 0/145 (0%)
 Strand=Plus/Plus

Query	1152	GGCCAAAGGCCGGGTACTCCAGGAGGCTCGAGTCCCATATAATCAGCAATGATGCTGC	1211
Sbjct	1514	GGCCAAAGGCCGGGTACTCCAGGAGGCTCGAGTCCCATATAATCAGCAATGATGCTGC	1573
Query	1212	AATGGCGCTGACTTCTATGGAAACAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCC	1271
Sbjct	1574	AATGGCGCTGACTTCTATGGAAACAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCC	1633
Query	1272	GAGGGTGGCATTGATGCCAGG	1296
Sbjct	1634	GAGGGTGGCATTGATGCCAGG	1658

Score = 193 bits (104), Expect = 3e-45
 Identities = 104/104 (100%), Gaps = 0/104 (0%)
 Strand=Plus/Plus

Query	1050	CTCACAGAACATCCAGCCTGTGTGCCCTCCAGCTGCCGCCAGGCCCTGGTGGATGGC	1109
Sbjct	1219	CTCACAGAACATCCAGCCTGTGTGCCCTCCAGCTGCCGCCAGGCCCTGGTGGATGGC	1278
Query	1110	AAGATCTGTACCGTGACGGCTGGGCAACACGCAGTACTATGG	1153
Sbjct	1279	AAGATCTGTACCGTGACGGCTGGGCAACACGCAGTACTATGG	1322

>gb|AC020907.6| Homo sapiens chromosome 19 clone CTD-2527I21, complete sequence
 Length=169891

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position

Score = 590 bits (319), Expect = 9e-165 Identities = 323/325 (99%), Gaps = 0/325 (0%) Strand=Plus/Plus			
Query	1459	AGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTCTCGCTGCG	1518
Sbjct	79750	AGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGACCGGTGGCTCTCGCTGCG	79809
Query	1519	CAGCCTCCAGGGCCGAGGTGATCCCGTGGTGGGATCCACGCTGGCCGAGGATGGGAC	1578
Sbjct	79810	CAGCCTCCAGGGCCGAGGTGATCCCGTGGTGGGATCCACGCTGGCCTAGGATGGGAC	79869
Query	1579	GTTTTCTCTTGGGCCGGTCCACAGGTCAAGGACACCCCTCCCTCAGGGTCCTCTCT	1638
Sbjct	79870	GTTTTCTCTTGGGCCGGTCCACAGGTCAAGGACACCCCTCCCTCAGGGTCCTCTCT	79929
Query	1639	TCCACAGTGCGGGCCCACTCAGCCCCGAGACCACCAACCTCACCCCTGACCCCCAT	1698
Sbjct	79930	TCCACAGTGCGGGCCCACTCAGCCCCGAGACCACCAACCTCACCCCTGACCCCCAT	79989
Query	1699	GTAAATATTGTTCTGCTGTCTGGACTCCCTGTCTAGGTGCCCTGATGATGGGATGCTCT	1758
Sbjct	79990	GTAAATATTGTTCTGCTGTCTGGACTCCCTGTCTAGGTGCCCTGATGACGGGATGCTCT	80049

Query 1759 TTAAATAATAAGATGGTTTGATT 1783
 Sbjct 80050 TTAAATAATAAGATGGTTTGATT 80074

Score = 353 bits (191), Expect = 1e-93
 Identities = 199/202 (98%), Gaps = 3/202 (1%)
 Strand=Plus/Plus

Query 858 TTCCT-GG-A-GCGAACGGGTCCTGTCCCAGTGGCAGTGTGCCCCGTGCCGTGGCC 914
 Sbjct 74119 TTCCCTGGTAGGCGAACGGGTCCTGTCCCAGTGGCAGTGTGCCCCGTGCCGTGGCC 74178

Query 915 CAGGCCTCTCCCCACGGTCTGCAGCTGGGGTGCAGGCTGTGGCTAACACGGGGCTAT 974
 Sbjct 74179 CAGGCCTCTCCCCACGGTCTGCAGCTGGGGTGCAGGCTGTGGCTAACACGGGGCTAT 74238

Query 975 CTTCCCTTCGGGACCCAAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCACCTC 1034
 Sbjct 74239 CTTCCCTTCGGGACCCAAACAGCGAGGAGAACAGCAACGATATTGCCCTGGTCCACCTC 74298

Query 1035 TCCAGTCCCCCTGCCCTCACAG 1056
 Sbjct 74299 TCCAGTCCCCCTGCCCTCACAG 74320

Score = 315 bits (170), Expect = 6e-82
 Identities = 172/173 (99%), Gaps = 0/173 (0%)
 Strand=Plus/Plus

Query 1288 CCTGCCAGGGCGACAGCGGTGGTCCCTTGTGTGAGGACAGCATCTCTCGGACGCCAC 1347
 Sbjct 79363 CCTCCCAGGGCGACAGCGGTGGTCCCTTGTGTGAGGACAGCATCTCTCGGACGCCAC 79422

Query 1348 GTTGGCGCTGTGTGGCATTGTGAGTTGGGACTGGCTGTGCCCTGGCCAGAACGCCAG 1407
 Sbjct 79423 GTTGGCGCTGTGTGGCATTGTGAGTTGGGACTGGCTGTGCCCTGGCCAGAACGCCAG 79482

Query 1408 GCGTCTACACCAAAGTCAGTGACTTCGGAGTGGATCTTCAGGCCATAAAG 1460
 Sbjct 79483 GCGTCTACACCAAAGTCAGTGACTTCGGAGTGGATCTTCAGGCCATAAAG 79535

Score = 313 bits (169), Expect = 2e-81
 Identities = 172/173 (99%), Gaps = 1/173 (0%)
 Strand=Plus/Plus

Query 695 CCA-AGACTGTGGCCGCAGGAAGCTGCCGTGGACCGCATCGTGGAGGCCGGACACCA 753
 Sbjct 73844 CCACAGACTGTGGCCGCAGGAAGCTGCCGTGGACCGCATCGTGGAGGCCGGACACCA 73903

Query 754 GCTTGGCCGGTGGCGTGGCAAGTCAGCCTTCGCTATGATGGAGGACACCTCTGTGGGG 813
 Sbjct 73904 GCTTGGCCGGTGGCGTGGCAAGTCAGCCTTCGCTATGATGGAGGACACCTCTGTGGGG 73963

Query 814 GATCCCTGCTCTCGGGGACTGGGTGCTGACAGCCGCCACTGCTTCCGGAG 866
 Sbjct 73964 GATCCCTGCTCTCGGGGACTGGGTGCTGACAGCCGCCACTGCTTCCGGAG 74016

Score = 289 bits (156), Expect = 4e-74
 Identities = 156/156 (100%), Gaps = 0/156 (0%)
 Strand=Plus/Plus

Query 38 CAGGTGAGGCAGGCTGGCCTAGCAGGCCACGCCACGGCTCTGCCCTCCAGGCCGGCC 97
 Sbjct 55222 CAGGTGAGGCAGGCTGGCCTAGCAGGCCACGCCACGGCTCTGCCCTCCAGGCCGGCC 55281

Query 98 CTGCTGGGGGCCACCATGCTCTGCCAGGCCACTGACCCGACCCGGCACTAC 157
 Sbjct 55282 CTGCTGGGGGCCACCATGCTCTGCCAGGCCACTGACCCGACCCGGCACTAC 55341

Query 158 CTCGAGGCTCCGCCCCCACCTGCTGGACCCAGGGT 193
 Sbjct 55342 CTCGAGGCTCCGCCCCCACCTGCTGGACCCAGGGT 55377

Score = 268 bits (145), Expect = 5e-68
 Identities = 145/145 (100%), Gaps = 0/145 (0%)
 Strand=Plus/Plus

Query 1152 GGCCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGC 1211
 Sbjct 79041 GGCCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGC 79100

Query 1212 AATGGCGCTGACTTCTATGGAAACCAGATCAAGCCAAGATGTTCTGTGCTGGCTACCC 1271
 Sbjct 79101 AATGGCGCTGACTTCTATGGAAACCAGATCAAGCCAAGATGTTCTGTGCTGGCTACCC 79160

Query 1272 GAGGGTGGCATTGATGCCAGG 1296
 Sbjct 79161 GAGGGTGGCATTGATGCCAGG 79185

Score = 248 bits (134), Expect = 6e-62
 Identities = 134/134 (100%), Gaps = 0/134 (0%)
 Strand=Plus/Plus

Query 403 CAGTGCAGGT CAGCTCTGGGACGCTGGCTCATGGCTTTGACAAGACGGAAGGGACGT 462
 Sbjct 73173 CAGTGCAGGT CAGCTCTGGGACGCTGGCTCATGGCTTTGACAAGACGGAAGGGACGT 73232
 Query 463 GGC GGCTGCTGTGCTCCTCGCGCTCCAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGA 522
 Sbjct 73233 GGC GGCTGCTGTGCTCCTCGCGCTCCAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGA 73292
 Query 523 TGGGCTTCCTCAGG 536
 Sbjct 73293 TGGGCTTCCTCAGG 73306

Score = 233 bits (126), Expect = 2e-57
 Identities = 129/130 (99%), Gaps = 1/130 (0%)
 Strand=Plus/Plus

Query 533 CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGGCCAATGGCACGTGGG 592
 Sbjct 73374 CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGGCCAATGGCACGTGGG 73433
 Query 593 CTTCTTCTGTGTGGACGAGGGAGGGCTGCCCCACACCCAGAGGCTGCTGGAGGTATCTC 652
 Sbjct 73434 CTTCTTCTGTGTGGACGAGGGAGGGCTGCCCCACACCCAGAGGCTGCTGGAGGTATCTC 73493
 Query 653 CGTGTG-TGA 661
 Sbjct 73494 CGTGTGGTGA 73503

Score = 193 bits (104), Expect = 3e-45
 Identities = 104/104 (100%), Gaps = 0/104 (0%)
 Strand=Plus/Plus

Query 1050 CTCACAGAATAACATCCAGGCCATGTGTGCCCTCCCAGCTGCCGCCAGGCCCTGGTGGATGGC 1109
 Sbjct 78746 CTCACAGAATAACATCCAGGCCATGTGTGCCCTCCCAGCTGCCGCCAGGCCCTGGTGGATGGC 78805
 Query 1110 AAGATCTGTACCGTGACGGGCTGGGCAACACGCAGTACTATGG 1153
 Sbjct 78806 AAGATCTGTACCGTGACGGGCTGGGCAACACGCAGTACTATGG 78849

Score = 191 bits (103), Expect = 1e-44
 Identities = 103/103 (100%), Gaps = 0/103 (0%)
 Strand=Plus/Plus

Query 261 GGTGGCCGGACTGTGCCATGCTGCTCAGACCCAAGGTGGCAGCTCTCACTGCCGGGACC 320
 Sbjct 62792 GGTGGCCGGACTGTGCCATGCTGCTCAGACCCAAGGTGGCAGCTCTCACTGCCGGGACC 62851
 Query 321 CTGCTACTTCTGACAGCCATCGGGCGGCATCCTGGGCCATTG 363
 Sbjct 62852 CTGCTACTTCTGACAGCCATCGGGCGGCATCCTGGGCCATTG 62894

Score = 137 bits (74), Expect = 1e-28
 Identities = 74/74 (100%), Gaps = 0/74 (0%)
 Strand=Plus/Plus

Query 191 GGTCCCACCCCTGGCCCAGGAGGT CAGCCAGGGAAATCTTAACAAGAGGCAGTGACATGGC 250
 Sbjct 55955 GGTCCCACCCCTGGCCCAGGAGGT CAGCCAGGGAAATCTTAACAAGAGGCAGTGACATGGC 56014
 Query 251 GCAGAAAGGAGGGTG 264
 Sbjct 56015 GCAGAAAGGAGGGTG 56028

Score = 82.4 bits (44), Expect = 7e-12
 Identities = 44/44 (100%), Gaps = 0/44 (0%)
 Strand=Plus/Plus

Query 1 TCGAGCCCGCTTCCAGGGACCCCTACCTGAGGGCCACAGGTGA 44
 Sbjct 54009 TCGAGCCCGCTTCCAGGGACCCCTACCTGAGGGCCACAGGTGA 54052

Score = 80.5 bits (43), Expect = 2e-11
 Identities = 43/43 (100%), Gaps = 0/43 (0%)
 Strand=Plus/Plus

Query 363 GTGGCTGTTCTCCTCAGGAGTGACCAGGAGCCGCTGTACCCAG 405
 Sbjct 62977 GTGGCTGTTCTCCTCAGGAGTGACCAGGAGCCGCTGTACCCAG 63019

Score = 78.7 bits (42), Expect = 9e-11
 Identities = 42/42 (100%), Gaps = 0/42 (0%)
 Strand=Plus/Plus

Query 658 GTGATTGCCCGAGAGGCCGTTCTGGCCGCCATCTGCCAAG 699
 Sbjct 73631 GTGATTGCCCGAGAGGCCGTTCTGGCCGCCATCTGCCAAG 73672

>dbj|AK125670.1| Homo sapiens cDNA FLJ43682 fis, clone TBAES2001258, weakly similar to SERINE PROTEASE HEPSIN (EC 3.4.21.-)
Length=2831

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 353 bits (191), Expect = 1e-93
Identities = 199/202 (98%), Gaps = 3/202 (1%)
Strand=Plus/Plus

Query	858	TTCCC-GG-A-GCGGAACGGGTCTGTCCCGATGGCGAGTGTGTTGCCGGTGCCGTGGCC	914
Sbjct	1437	TTCCCTGGTAGGCAGAACGGGTCTGTCCCGATGGCGAGTGTGTTGCCGGTGCCGTGGCC	1496
Query	915	CAGGCCTCTCCCA CGGTCTGCAGCTGGGGTGCAGGCTGTGGCTAACACGGGGCTAT	974
Sbjct	1497	CAGGCCTCTCCCA CGGTCTGCAGCTGGGGTGCAGGCTGTGGCTAACACGGGGCTAT	1556
Query	975	CTTCCTTTCGGGACCCAACAGCGAGGAGAACAGAACGATATTGCCCTGGTCCACCTC	1034
Sbjct	1557	CTTCCTTTCGGGACCCAACAGCGAGGAGAACAGAACGATATTGCCCTGGTCCACCTC	1616
Query	1035	TCCAGTCCCCCTGCCCTCACAG 1056	
Sbjct	1617	TCCAGTCCCCCTGCCCTCACAG 1638	

Score = 313 bits (169), Expect = 2e-81
Identities = 172/173 (99%), Gaps = 1/173 (0%)
Strand=Plus/Plus

Query	695	CCA-AGACTGTGGCCGCAGGAAGCTGCCGTGGACCGCATCGTGGGAGGCCGGGACACCA	753
Sbjct	1162	CCACAGACTGTGGCCGCAGGAAGCTGCCGTGGACCGCATCGTGGGAGGCCGGGACACCA	1221
Query	754	GCTTGGGCCGGTGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGG	813
Sbjct	1222	GCTTGGGCCGGTGGCCGTGGCAAGTCAGCCTTCGCTATGATGGAGCACACCTCTGTGGGG	1281
Query	814	GATCCCTGCTCTCCGGGGACTGGGTGCTGACAGCCGCCACTGCTCCCGGAG 866	
Sbjct	1282	GATCCCTGCTCTCCGGGGACTGGGTGCTGACAGCCGCCACTGCTCCCGGAG 1334	

Score = 248 bits (134), Expect = 6e-62
Identities = 134/134 (100%), Gaps = 0/134 (0%)
Strand=Plus/Plus

Query	403	CAGTGCAGGTCA GCTCTGCCGACGCTCGGCTCATGGCTTTGACAAGACGGAAGGGACGT	462
Sbjct	490	CAGTGCAGGTCA GCTCTGCCGACGCTCGGCTCATGGCTTTGACAAGACGGAAGGGACGT	549
Query	463	GGCGGCTGCTGTGCTCCTCGCGCTCAAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGA	522
Sbjct	550	GGCGGCTGCTGTGCTCCTCGCGCTCAAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGA	609
Query	523	TGGGCTTCTCAGG 536	
Sbjct	610	TGGGCTTCTCAGG 623	

Score = 233 bits (126), Expect = 2e-57
Identities = 129/130 (99%), Gaps = 1/130 (0%)
Strand=Plus/Plus

Query	533	CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCAAATGGCACGTCGGG	592
Sbjct	691	CAGGGCACTGACCCACTCCGAGCTGGACGTGCGAACGGCGGGCGCAAATGGCACGTCGGG	750
Query	593	CTTCTTCTGTGGACGAGGGGAGGCTGCCACACCCAGAGGCTGCTGGAGGTATCTC	652
Sbjct	751	CTTCTTCTGTGGACGAGGGGAGGCTGCCACACCCAGAGGCTGCTGGAGGTATCTC	810
Query	653	CGTGTG-TGA 661	
Sbjct	811	CGTGTGGTGA 820	

Score = 78.7 bits (42), Expect = 9e-11
Identities = 42/42 (100%), Gaps = 0/42 (0%)
Strand=Plus/Plus

Query	658	GTGATTGCCCAAGAGGCCGTTCTGGCCGCATCTGCCAAG 699	
Sbjct	948	GTGATTGCCCAAGAGGCCGTTCTGGCCGCATCTGCCAAG 989	

>gb|DQ677665.1| Homo sapiens sodium channel beta-1 subunit precursor (SCN1B)
gene, complete cds
Length=15819

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 289 bits (156), Expect = 4e-74
 Identities = 156/156 (100%), Gaps = 0/156 (0%)
 Strand=Plus/Plus

Query 38	CAGGTGAGGCAGCCTGGCCTAGCAGGCCACGCCACCGCCTCTGCCCTCCAGGCCCGCG 97
Sbjct 14090	CAGGTGAGGCAGCCTGGCCTAGCAGGCCACGCCACCGCCTCTGCCCTCCAGGCCCGCG 14149
Query 98	CTGCTGCGGGGCCACCATGCTCCTGCCAGGCCACTGAGACTGACCCGACCCGGCACTAC 157
Sbjct 14150	CTGCTGCGGGGCCACCATGCTCCTGCCAGGCCACTGAGACTGACCCGACCCGGCACTAC 14209
Query 158	CTCGAGGCTCCGCCCCCACCTGCTGGACCCAGGGT 193
Sbjct 14210	CTCGAGGCTCCGCCCCCACCTGCTGGACCCAGGGT 14245

Score = 137 bits (74), Expect = 1e-28
 Identities = 74/74 (100%), Gaps = 0/74 (0%)
 Strand=Plus/Plus

Query 191	GGTCCCACCCCTGGCCAGGAGGTAGCCAGGAATCATTAACAAGAGGCAGTGACATGGC 250
Sbjct 14823	GGTCCCACCCCTGGCCAGGAGGTAGCCAGGAATCATTAACAAGAGGCAGTGACATGGC 14882
Query 251	GCAGAAGGAGGGTG 264
Sbjct 14883	GCAGAAGGAGGGTG 14896

Score = 82.4 bits (44), Expect = 7e-12
 Identities = 44/44 (100%), Gaps = 0/44 (0%)
 Strand=Plus/Plus

Query 1	TCGAGCCCGCTTCCAGGGACCCTACCTGAGGGCCACAGGTGA 44
Sbjct 12877	TCGAGCCCGCTTCCAGGGACCCTACCTGAGGGCCACAGGTGA 12920

>gb|AC197610.3| MACACA MULATTA BAC clone CH250-348G8 from chromosome 19, complete sequence
 Length=158733

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position

Score = 250 bits (135), Expect = 2e-62
 Identities = 149/156 (95%), Gaps = 0/156 (0%)
 Strand=Plus/Plus

Query 38	CAGGTGAGGCAGCCTGGCCTAGCAGGCCACGCCACCGCCTCTGCCCTCCAGGCCCGCG 97
Sbjct 149463	CAGGTGAGGCAGCCTGGCCTAGCAGGCCACGCCACCGCCTCTGCCCTCCAGGCCACCG 149522
Query 98	CTGCTGCGGGGCCACCATGCTCCTGCCAGGCCACTGAGACTGACCCGACCCGGCACTAC 157
Sbjct 149523	CTGCTGCGGGGCCACCATGCTCCTGCCAGGCCACTGAGACTGACCCGACCCGGAAACCAC 149582
Query 158	CTCGAGGCTCCGCCCCCACCTGCTGGACCCAGGGT 193
Sbjct 149583	CTCCAGGCTCCGCCCTCACCTGCCAGGCCAGGGT 149618

Score = 180 bits (97), Expect = 2e-41
 Identities = 101/103 (98%), Gaps = 0/103 (0%)
 Strand=Plus/Plus

Query 261	GGTGGCCGGACTGTGCCATGCTGCCAGACCCAAGGTGGCAGCTCTCACTGCGGGGACC 320
Sbjct 157187	GGTGGCCGGACTGTGCCATGCTGCCAGACCCAAGGTGGCAGCTCTCACTGCGGGGACC 157246
Query 321	CTGCTACTTCTGACAGCCATCGGGCGGCATCCTGGGCCATTG 363
Sbjct 157247	CTGCTACTTCTGACAGCCATCGGGCGGCATCCTGGGCCATTG 157289

Score = 132 bits (71), Expect = 6e-27
 Identities = 73/74 (98%), Gaps = 0/74 (0%)
 Strand=Plus/Plus

Query 191	GGTCCCACCCCTGGCCAGGAGGTAGCCAGGAATCATTAACAAGAGGCAGTGACATGGC 250
Sbjct 150194	GGTCCCACCCCTGGCCAGGAGGTAGCCAGGAATCATTAACAAGAGGCAGTGACATGGC 150253
Query 251	GCAGAAGGAGGGTG 264
Sbjct 150254	GCAGAAGGAGGGTG 150267

Score = 75.0 bits (40), Expect = 1e-09
 Identities = 42/43 (97%), Gaps = 0/43 (0%)
 Strand=Plus/Plus

Query 363	GTGGCTGTTCTCCTCAGGAGGTAGCAGGCCAGGGCTGTACCCAG 405
Sbjct 157372	GTGGCTGTTCTCCTCAGGAGGTAGCAGGCCAGGGCTGTACCCAG 157414

>ref|XM_001719305.1| PREDICTED: Homo sapiens hypothetical protein LOC100128675 (LOC100128675), mRNA Length=1287

Score = 207 bits (112), Expect = 1e-49
 Identities = 112/112 (100%), Gaps = 0/112 (0%)
 Strand=Plus/Minus

Query	403	CAGTGCAGGTCAAGCTCTGGGACGCTCGGCTCATGGTCTTGACAAGACGGAAAGGGACGT	462
Sbjct	513	CAGTGCAGGTCAAGCTCTGGGACGCTCGGCTCATGGTCTTGACAAGACGGAAAGGGACGT	454
Query	463	GGCGGCTGCTGTGCTCCTCGCCTCCAAAGCCAGGGTAGCCGGACTCAGCTG	514
Sbjct	453	GGCGGCTGCTGTGCTCCTCGCCTCCAAAGCCAGGGTAGCCGGACTCAGCTG	402

>ref|XM_001721961.1| PREDICTED: Homo sapiens hypothetical protein LOC100128675 (LOC100128675), mRNA Length=1287

Score = 207 bits (112), Expect = 1e-49
 Identities = 112/112 (100%), Gaps = 0/112 (0%)
 Strand=Plus/Minus

Query	403	CAGTGCAGGTCAAGCTCTGGGACGCTCGGCTCATGGTCTTGACAAGACGGAAAGGGACGT	462
Sbjct	513	CAGTGCAGGTCAAGCTCTGGGACGCTCGGCTCATGGTCTTGACAAGACGGAAAGGGACGT	454
Query	463	GGCGGCTGCTGTGCTCCTCGCCTCCAAAGCCAGGGTAGCCGGACTCAGCTG	514
Sbjct	453	GGCGGCTGCTGTGCTCCTCGCCTCCAAAGCCAGGGTAGCCGGACTCAGCTG	402

>ref|XM_001719287.1| PREDICTED: Homo sapiens hypothetical protein LOC100128675 (LOC100128675), mRNA Length=1287

Score = 207 bits (112), Expect = 1e-49
 Identities = 112/112 (100%), Gaps = 0/112 (0%)
 Strand=Plus/Minus

Query	403	CAGTGCAGGTCAAGCTCTGGGACGCTCGGCTCATGGTCTTGACAAGACGGAAAGGGACGT	462
Sbjct	513	CAGTGCAGGTCAAGCTCTGGGACGCTCGGCTCATGGTCTTGACAAGACGGAAAGGGACGT	454
Query	463	GGCGGCTGCTGTGCTCCTCGCCTCCAAAGCCAGGGTAGCCGGACTCAGCTG	514
Sbjct	453	GGCGGCTGCTGTGCTCCTCGCCTCCAAAGCCAGGGTAGCCGGACTCAGCTG	402

>gb|AC158993.2| Mus musculus BAC clone RP24-427N13 from chromosome 7, complete sequence Length=179746

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position

Score = 141 bits (76), Expect = 1e-29
 Identities = 122/145 (84%), Gaps = 0/145 (0%)
 Strand=Plus/Minus

Query	1152	GGCCAACAGGCCGGGTACTCCAGGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGC	1211
Sbjct	61803	GGCCAACAGGCCGTATGGTGCTCCAAGAGGCCGGTTCCCATCATAAGCAACGAAGTTGC	61744
Query	1212	AATGGCGCTGACTTCTATGGAAACCAGATCAAGCCAAGATGTTCTGTGCTGGCTACCCC	1271
Sbjct	61743	AACAGCCCCGACTTCTACGGGAATCAGATCAAGCCAAGATGTTCTGTGCTGGCTATCCT	61684
Query	1272	GAGGGTGGCATTGATGCCAGG	1296
Sbjct	61683	GAGGGTGGCATTGATGCCAGG	61659

Score = 119 bits (64), Expect = 5e-23
 Identities = 92/105 (87%), Gaps = 4/105 (3%)
 Strand=Plus/Minus

Query	261	GGTGGCCGGACTG-TGCCATGCTGCCAGACCCAAGGTGGCAGCTCTCACTGCCGGGAC	319
Sbjct	71347	GGTGGCCGGACTGCAAGCTGCCAGACCCAAGGTGGCAGCTCTCACTGCCGGGAC	71289
Query	320	CCTGCTACTTC-TGACAGCCATCGGGCGGCATCTGGGCCATTG	363
Sbjct	71288	CCTGCTG-TTCCTGACAGGCATTGGGCCGCTGGGCCATTG	71245

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
Posted date: May 19, 2008 5:44 PM
Number of letters in database: -2,000,849,822
Number of sequences in database: 6,839,787

Lambda K H
1.33 0.621 1.12
Gapped
Lambda K H
1.33 0.621 1.12
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 6839787
Number of Hits to DB: 3671278
Number of extensions: 17
Number of successful extensions: 17
Number of sequences better than 10: 3
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 16
Number of HSP's successfully gapped: 16
Length of query: 1783
Length of database: 23768953950
Length adjustment: 33
Effective length of query: 1750
Effective length of database: 23543240979
Effective search space: 41200671713250
Effective search space used: 41200671713250
A: 0
X1: 15 (28.8 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 15 (28.8 bits)
S2: 23 (43.6 bits)